

GenCore version 5.1.7  
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OM protein - protein search, using sw model  
Run on: April 11, 2006, 02:03:38 ; Search time 112.845 Seconds  
(without alignments)  
1608.075 Million cell updates/sec

Title: US-09-037-657-13  
Perfect score: 2251  
Sequence: 1 MPAGRPGVQAQSRPPRPL.....WRAMQKSHKTRNQVLPAKL 413

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2251	100.0	413	2 AAW55011	Novel hae
2	2251	100.0	413	3 AAY93658	Aay93658 A murine
3	2251	100.0	413	4 AAS00820	Aae00820 Murine ha
4	2226.5	98.9	425	2 AAW55012	Novel hae
5	2226.5	98.9	425	3 AAY93659	Aay93659 A murine
6	2226.5	98.9	425	4 AAS00821	Murine ha
7	2222.5	98.7	425	2 AAW59804	Nucleotid
8	2222.5	98.7	425	2 AAY26337	Murine U4
9	2197.5	97.6	425	2 AAW70862	Rat Zcyto
10	2134.5	94.8	416	2 AAY29780	Mouse DNA
11	2119	94.1	407	3 AAB19589	Mouse cyt
12	2119	94.1	407	4 AAB36648	Mouse cyt
13	2119	94.1	407	7 ADC07180	Mouse cyt
14	2119	94.1	407	8 ADT90845	Mouse cyt
15	2119	94.1	407	8 ADT61033	Mouse cyt
16	2119	94.1	407	9 ADT57158	Mouse cyt
17	2119	94.1	407	9 ADT65015	Mouse NR6
18	2118.5	94.1	405	2 AAY15214	Amino aci
19	2118.5	94.1	405	3 AAY44839	Mouse orp
20	2114.5	93.9	410	2 AAY29779	Human DNA
21	2114.5	93.9	410	3 AAB19588	Human cyt
22	2114.5	93.9	410	4 AAB36647	Human cyt
23	2114.5	93.9	410	7 ADC07179	Human cyt
24	2114.5	93.9	410	8 ADT90844	Human cyt

25	2114.5	93.9	410	8 ADT61032	Human cyt
26	2114.5	93.9	410	9 ADY57157	Human cyt
27	2114.5	93.9	410	9 ADZ65014	Human NR6
28	2098	93.2	425	2 AAW70861	Allelic v
29	2097.5	93.2	421	4 AAE00826	Murine ha
30	2096.5	93.1	426	2 AAY28281	Amino aci
31	2096	93.1	422	2 AAY05782	Human typ
32	2096	93.1	422	2 AAY06479	Human tum
33	2096	93.1	422	2 AAY17825	Human PRO
34	2096	93.1	422	2 AAY26339	Human U4
35	2096	93.1	422	3 AAB01316	Human PRO
36	2096	93.1	422	3 AAY93686	Amino aci
37	2096	93.1	422	4 AAG63545	Amino aci
38	2096	93.1	422	6 ABUS5925	Human sec
39	2096	93.1	422	6 ABUS60235	Human PRO
40	2096	93.1	422	6 ABG72776	Human cyt
41	2096	93.1	422	6 ABU64921	Human sec
42	2096	93.1	422	6 ABUS8355	Novel hum
43	2096	93.1	422	6 ABUS7241	Human PRO
44	2096	93.1	422	6 ABUS6306	Human sec
45	2096	93.1	422	6 ABUS60346	Novel hum

ALIGNMENTS

RESULT 1  
AAW55011  
ID AAW55011 standard; protein; 413 AA.  
XX AC AAW55011;  
XX DT 29-SEP-1998 (first entry)  
XX DE Novel haemopoietin receptor NR6.1 protein.  
XX KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;  
KW cell survival; therapeutic; neuronal proliferation; drug screening;  
KW Mouse.  
XX OS Mus sp.  
XX FN WO9811225-A2.  
XX PD 19-MAR-1998.  
XX PF 11-SEP-1997; 97WO-GB002479.  
XX PR 11-SEP-1996; 96AU-00002246.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX (DZIE/) DZIEGLEWSKA H E.  
XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;  
PI Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;  
DR WPI: 1998-260970/23.  
DR N-PSDB; AAV27140.  
XX New isolated haemopoietin receptor - used for developing products for  
PT modulating proliferation, differentiation and survival of cells, e.g.  
XX neuronal cells.  
XX Claim 14; Page 77-81; 182pp; English.  
XX The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.  
CC Interaction between the novel HR and a ligand facilitates proliferation,  
CC differentiation and survival of a wide variety of cells. The HR and it's  
CC derivatives can be used for modulating the activity of the receptors e.g.  
CC to regulate development, maintenance or regeneration in an array of  
CC different cells and tissues in vitro and in vivo. They can be present in  
CC therapeutics used for modulating neuronal proliferation, differentiation  
CC and survival. The products can also be used for detection and diagnosis,

CC e.g. for cancers or predisposition to cancers, or for drug screening  
 XX SQ Sequence 413 AA;

Query Match 100.0%; Score 2251; DB 2; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-186;  
 Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSIQ 60  
 |||||  
 DB 1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSIQ 60  
 |||||

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 |||||  
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 |||||

QY 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 |||||  
 DB 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 |||||

QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVDDVTTDP 240  
 |||||  
 DB 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVDDVTTDP 240  
 |||||

QY 241 PPDVHVSRYGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300  
 |||||  
 DB 241 PPDVHVSRYGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300  
 |||||

QY 301 LAGLKPGTVYFVQVRCNPGIYGSKKAGIWESEWSPHTAASSTPRSERPGGGVCEPRGGE 360  
 |||||  
 DB 301 LAGLKPGTVYFVQVRCNPGIYGSKKAGIWESEWSPHTAASSTPRSERPGGGVCEPRGGE 360  
 |||||

QY 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAKL 413  
 |||||  
 DB 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAKL 413  
 |||||

RESULT 2  
 AAY93658  
 ID AAY93658 standard; protein; 413 AA.  
 XX AC AAY93658;  
 XX AC AAY93658;  
 XX DT 25-SEP-2000 (first entry)  
 XX DE A murine hemopoietin receptor NR6.1 polypeptide.  
 XX KW Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;  
 XX KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;  
 XX KW suckling; postnatal baby; foetal testing.  
 XX OS Mus musculus.  
 XX PN WO200035471-A1.  
 XX XX  
 XX PD 22-JUN-2000.  
 XX PF 17-DEC-1999; 99WO-AU001119.  
 XX PR 17-DEC-1998; 98AU-00007762.  
 XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 XX PI Alexander WS, Metcalf D;  
 XX DR WPI; 2000-442273/38.  
 XX DR N-PSDB; AAA46791.  
 XX XX  
 XX PT Administering the hemopoietin receptor NR6 is used to modulate production  
 XX PT of hemopoietic progenitor cells and facilitate postnatal survival of  
 XX PT mammals by inducing or promoting suckling.  
 XX XX  
 XX PS Claim 5; Page 70-71; 77pp; English.

XX The present sequence represents a murine haemopoietin receptor NR6 (CLF-  
 CC 1) polypeptide. The specification describes a method for the treatment or  
 CC prophylaxis of disease conditions associated with dysfunctional  
 CC haemopoietic regulation. The method comprises modulating the production  
 CC of hemopoietic progenitor cells in a mammal by administration of NR6.  
 CC Decreasing production of progenitor cells may be used in the treatment of  
 CC cancer or to induce apoptosis of particular cell types. Increasing  
 CC production of progenitor cells is used to facilitate postnatal survival  
 CC in mammals by inducing or promoting suckling. Potential disease  
 CC conditions may be identified by monitoring NR6 production in postnatal  
 CC babies or allowing expectant mothers to undergo foetal testing. Low NR6  
 CC levels can then be treated immediately  
 XX SQ Sequence 413 AA;

Query Match 100.0%; Score 2251; DB 3; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-186;  
 Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSIQ 60  
 |||||  
 DB 1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSIQ 60  
 |||||

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 |||||  
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 |||||

QY 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 |||||  
 DB 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 |||||

QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVDDVTTDP 240  
 |||||  
 DB 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVDDVTTDP 240  
 |||||

QY 241 PPDVHVSRYGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300  
 |||||  
 DB 241 PPDVHVSRYGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300  
 |||||

QY 301 LAGLKPGTVYFVQVRCNPGIYGSKKAGIWESEWSPHTAASSTPRSERPGGGVCEPRGGE 360  
 |||||  
 DB 301 LAGLKPGTVYFVQVRCNPGIYGSKKAGIWESEWSPHTAASSTPRSERPGGGVCEPRGGE 360  
 |||||

QY 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAKL 413  
 |||||  
 DB 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAKL 413  
 |||||

RESULT 3  
 AAE00820  
 ID AAE00820 standard; protein; 413 AA.  
 XX AC AAE00820;  
 XX AC AAE00820;  
 XX DT 09-SEP-2004 (revised)  
 XX DT 02-JUL-2001 (first entry)  
 XX XX  
 XX DE Murine haemopoietin receptor, NR6.1 isoform.  
 XX KW Murine; biologically active complex; haemopoietin receptor; NR6;  
 XX KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;  
 XX KW differentiation; cell survival; neurotrophic activity.  
 XX OS Mus sp.  
 XX OS Unidentified.  
 XX XX  
 XX FH Key Location/Qualifiers  
 XX FT Domain 330..334  
 XX FT /label = WSXWS\_motif  
 XX XX  
 XX PN WO200127157-A1.

PD 19-APR-2001.  
 XX  
 XX 06-OCT-2000; 2000WO-AU001216.  
 XX  
 XX 08-OCT-1999; 99AU-00003327.  
 PR 12-MAY-2000; 2000AU-00007489.  
 XX  
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PA  
 XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;  
 PI Nakata Y, Hasegawa M;  
 XX  
 XX WPI: 2001-281978/29.  
 DR N-PSDB; AAD04192.  
 XX  
 XX New biologically active complex comprising NR6 and cardiotrophin-like-  
 PT cytokine, for facilitating proliferation, differentiation and/or survival  
 PT of a cell.  
 XX  
 XX Claim 25; Page 76-77; 123pp; English.  
 PS  
 XX The present invention relates to a biologically active complex comprising  
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The  
 CC complex is useful in the manufacture of a medicament for the treatment  
 CC and/or prophylaxis of a subject, as it is involved in facilitating  
 CC proliferation, differentiation and/or survival of a cell. The complex or  
 CC its components have neurotrophic activity. The present sequence is murine  
 CC haemopoietin receptor, NR6.1 isoform. The NR6.1 represents the NR6 splice  
 CC variant obtained due to alternative mRNA splicing  
 CC  
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key  
 XX  
 XX Sequence 413 AA;

Query Match 100.0%; Score 2251; DB 4; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-186; Mismatches 0; Indels 0; Gaps 0;  
 Matches 413; Conservative 0;  
 QY 1 MPAGRPGVQAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60  
 DB 1 MPAGRPGVQAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60  
 QY 61 ATCSIHGDTPGATAGLYWTNLGRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTNLGRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 QY 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240  
 DB 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240  
 QY 241 PPDVHVS RVGLEDQLSVRWVSPPALKDPLFQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
 DB 241 PPDVHVS RVGLEDQLSVRWVSPPALKDPLFQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
 QY 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
 DB 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLVDQWRAWMQKSHKTRNOVLPAKL 413  
 DB 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLVDQWRAWMQKSHKTRNOVLPAKL 413

## RESULT 4

AAW55012  
 ID AAW55012 standard; protein; 425 AA.

XX  
 AC AAW55012;  
 XX

DT 29-SEP-1998 (first entry)  
 XX  
 XX Novel haemopoietin receptor NR6.2 protein.  
 XX  
 KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;  
 KW cell survival; therapeutic; neuronal proliferation; drug screening;  
 KW Mouse.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9811225-A2.  
 PN  
 XX 19-MAR-1998.  
 XX  
 XX 11-SEP-1997; 97WO-GB002479.  
 PF  
 XX 11-SEP-1996; 96AU-00002246.  
 PR  
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX (DZIE/) DZIEGLEWSKA H E.  
 PA  
 XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;  
 PI Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;  
 XX  
 DR WPI: 1998-260970/23.  
 DR N-PSDB; AAV27141.  
 XX  
 XX New isolated haemopoietin receptor - used for developing products for  
 PT modulating proliferation, differentiation and survival of cells, e.g.  
 PT neuronal cells.  
 XX  
 XX Claim 15; Page 84-87; 182pp; English.  
 PS  
 XX The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.  
 CC Interaction between the novel HR and a ligand facilitates proliferation,  
 CC differentiation and survival of a wide variety of cells. The HR and its  
 CC derivatives can be used for modulating the activity of the receptors e.g.  
 CC to regulate development, maintenance or regeneration in an array of  
 CC different cells and tissues in vitro and in vivo. They can be present in  
 CC therapeutics used for modulating neuronal proliferation, differentiation  
 CC and survival. The products can also be used for detection and diagnosis,  
 CC e.g. for cancers or predisposition to cancers, or for drug screening  
 XX  
 XX Sequence 425 AA;

Query Match 98.9%; Score 2226.5; DB 2; Length 425;  
 Best Local Similarity 98.8%; Pred. No. 3.5e-184;  
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;  
 QY 1 MPAGRPGVQAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60  
 DB 1 MPAGRPGVQAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60  
 QY 61 ATCSIHGDTPGATAGLYWTNLGRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTNLGRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 QY 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240  
 DB 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240  
 QY 241 PPDVHVS RVGLEDQLSVRWVSPPALKDPLFQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
 DB 241 PPDVHVS RVGLEDQLSVRWVSPPALKDPLFQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
 QY 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
 DB 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360

QY 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411  
 DB 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNDEGILPS 414

RESULT 5  
 ID AAY93659 standard; protein; 425 AA.  
 AC AAY93659;  
 DT 25-SEP-2000 (first entry)  
 DE A murine hemopoietin receptor NR6.2 polypeptide.  
 KW Hemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;  
 KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;  
 KW suckling; postnatal baby; foetal testing.  
 OS Mus musculus.  
 PN WO200035471-A1.  
 PD 22-JUN-2000.  
 PF 17-DEC-1999; 99WO-AU001119.  
 PR 17-DEC-1998; 98AU-00007762.  
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 PI Alexander WS, Metcalf D;  
 DR WPI: 2000-442273/38.  
 DR N-PSDB; AAR46792.  
 XX Administering the hemopoietin receptor NR6 is used to modulate production  
 of hemopoietic progenitor cells and facilitate postnatal survival of  
 mammals by inducing or promoting suckling.  
 PS Claim 5; Page 73-74; 77pp; English.

The present sequence represents a murine haemopoietin receptor NR6 (CLF-1) polypeptide. The specification describes a method for the treatment or prophylaxis of disease conditions associated with dysfunctional haemopoietic regulation. The method comprises modulating the production of hemopoietic progenitor cells in a mammal by administration of NR6. Decreasing production of progenitor cells may be used in the treatment of cancer or to induce apoptosis of particular cell types. Increasing production of progenitor cells is used to facilitate postnatal survival in mammals by inducing or promoting suckling. Potential disease conditions may be identified by monitoring NR6 production in postnatal babies or allowing expectant mothers to undergo foetal testing. Low NR6 levels can then be treated immediately

Query Match 98.9%; Score 2226.5; DB 3; Length 425;  
 Best Local Similarity 98.8%; Pred. No. 3.5e-184;  
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRGPGVAQARRPRPLSLWSPLLLCVLGPVGGGAHTAVISPDPTLLIGSSLQ 60  
 DB 1 MPAGRGPGVAQARRPRPLSLWSPLLLCVLGPVGGGAHTAVISPDPTLLIGSSLQ 60

QY 61 ATCSIHGDTPGAETAGLYWTLNGRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGAETAGLYWTLNGRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLVGLPPEKPNISCSWRNNKDLTCRWTPGAGETFLHTNYSILKYKLWR 180  
 DB 121 ARDGSILAGSCLVGLPPEKPNISCSWRNNKDLTCRWTPGAGETFLHTNYSILKYKLWR 180

QY 191 YGQDNTCEYHTVGHPSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTDDP 240  
 DB 191 YGQDNTCEYHTVGHPSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTDDP 240

QY 241 PPDVHVSRVGGLEDQLSVRWVSPPALKDPLFQAKYQIRYVEDSVDMKWVDDVSNQTSR 300  
 DB 241 PPDVHVSRVGGLEDQLSVRWVSPPALKDPLFQAKYQIRYVEDSVDMKWVDDVSNQTSR 300

QY 301 LAGLKPQGTIVYFVQRCNPFGIYGSKKAGIWEWSHPTAASPRSRPGGVCPRGGE 360  
 DB 301 LAGLKPQGTIVYFVQRCNPFGIYGSKKAGIWEWSHPTAASPRSRPGGVCPRGGE 360

QY 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411  
 DB 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNDEGILPS 414

RESULT 6  
 ID AAE00821 standard; protein; 425 AA.  
 XX AAE00821;  
 DT 09-SEP-2004 (revised)  
 DT 02-JUL-2001 (first entry)  
 XX Murine haemopoietin receptor, NR6.2 isoform.  
 KW Murine; biologically active complex; haemopoietin receptor; NR6;  
 KW cardiostrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;  
 KW differentiation; cell survival; neurotrophic activity.  
 OS Mus sp.  
 OS Unidentified.  
 FH Key Location/Qualifiers  
 FT Domain 330..334  
 FT /label = WSXWS\_motif  
 XX WO200127157-A1.  
 XX 19-APR-2001.  
 XX 06-OCT-2000; 2000WO-AU001216.  
 XX 08-OCT-1999; 99AU-00003327.  
 PR 12-MAY-2000; 2000AU-00007489.  
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PA Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;  
 PI Nakata Y, Hasegawa M;  
 XX WPI: 2001-281978/29.  
 DR N-PSDB; AAD04193.  
 XX New biologically active complex comprising NR6 and cardiostrophin-like  
 cytokine, for facilitating proliferation, differentiation and/or survival  
 of a cell.  
 PS Claim 26; Page 81-83; 123pp; English.

The present invention relates to a biologically active complex comprising a haemopoietin receptor, NR6 and cardiostrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is murine haemopoietin receptor, NR6.2 isoform. The NR6.2 represents the NR6 splice variant obtained due to alternative mRNA splicing

Revised record issued on 09-SEP-2004 : Correction to Feature Table Key

SQ Sequence 425 AA;

Query Match 98.9%; Score 2226.5; DB 4; Length 425;  
 Best Local Similarity 98.8%; Pred. No. 3.5e-184;  
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRPGVQAQARRPRPLSLWSPLLCVLGVRGGSGAHTAVISPDPTLLIGSSLQ 60  
 DB 1 MPAGRPGVQAQARRPRPLSLWSPLLCVLGVRGGSGAHTAVISPDPTLLIGSSLQ 60

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTDP 240  
 DB 181 YQDNTCEYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTDP 240

QY 241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCK 300  
 DB 241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCK 300

QY 301 LAGLKPGTVYFVQVRCNPFYIGYKAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360  
 DB 301 LAGLKPGTVYFVQVRCNPFYIGYKAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360

QY 361 PSSGPVRRLEKQFLGWLKCHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
 DB 361 PSSGPVRRLEKQFLGWLKCHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 7  
 AAW59804  
 ID AAW59804 standard; protein; 425 AA.  
 AC AAW59804;  
 DT 26-OCT-1998 (first entry)  
 DE Nucleotide sequence of the murine U4 protein.  
 KW Murine; U4 protein; haematopoietin receptor superfamily;  
 KW cell proliferation; immune response; antibody; cell differentiation;  
 KW autoimmune disease; cancer; allergy.  
 OS Mus sp.  
 PN WO9831811-A1.  
 PD 23-JUL-1998.  
 PF 15-JAN-1998; 98WO-US000334.  
 PR 16-JAN-1997; 97US-00784863.  
 PA (GENY ) GENETICS INST INC.  
 PI Donaldson DD, Collins M, Neben T, Whitters M;  
 DR WPI; 1998-414109/35.  
 DR N-PSDB; AAV41688.  
 XX New nucleic acid encoding U4 haematopoietin receptor superfamily chain -  
 PT potentially useful, e.g. for modulating cell proliferation or immune  
 PT response, for treating cancer and auto-immune disease.  
 XX Claim 9; Page 26-27; 38pp; English.  
 XX This is the amino acid sequence of the murine U4 protein from the

CC haematopoietin receptor superfamily, used in the method of the invention  
 CC for the modulation of cell proliferation, or the immune response.  
 CC Transformed mammalian cells are used to produce recombinant U4 protein.  
 CC The U4 protein is used to screen for specific binding agents, raise  
 CC antibodies. It is also used as reagents for assays and as tissue markers  
 CC for isolation of cognate ligands and receptors, and in pharmaceutical  
 CC compositions which may modulate cell proliferation, cell differentiation,  
 CC and the immune system (e.g. for treating immune deficiency, inherited or  
 CC the result of infection, autoimmune diseases, cancer, and allergy)  
 XX SQ Sequence 425 AA;

Query Match 98.7%; Score 2222.5; DB 2; Length 425;  
 Best Local Similarity 98.6%; Pred. No. 7.8e-184;  
 Matches 408; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 MPAGRPGVQAQARRPRPLSLWSPLLCVLGVRGGSGAHTAVISPDPTLLIGSSLQ 60  
 DB 1 MPAGRPGVQAQARRPRPLSLWSPLLCVLGVRGGSGAHTAVISPDPTLLIGSSLQ 60

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTDP 240  
 DB 181 YQDNTCEYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTDP 240

QY 241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCK 300  
 DB 241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCK 300

QY 301 LAGLKPGTVYFVQVRCNPFYIGYKAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360  
 DB 301 LAGLKPGTVYFVQVRCNPFYIGYKAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360

QY 361 PSSGPVRRLEKQFLGWLKCHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
 DB 361 PSSGPVRRLEKQFLGWLKCHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 8  
 AAY26337  
 ID AAY26337 standard; protein; 425 AA.  
 AC AAY26337;  
 DT 13-JAN-2000 (first entry)  
 DE Murine U4 haematopoietin receptor superfamily chain.  
 KW Murine U4 protein; haematopoietin receptor superfamily;  
 KW biological activity; cytokine; cell proliferation; cell differentiation;  
 KW immune stimulation; immune suppression; haematopoiesis regulation;  
 KW immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;  
 KW myeloid cell; lymphoid cell deficiency; platelet disorder.  
 OS Mus sp.  
 FH Key  
 FT Peptide 1.40  
 FT /label= Putative\_signal\_sequence  
 FT Protein 41.383  
 FT /label= Mature\_murine\_U4  
 XX WO9953066-A1.  
 XX 21-OCT-1999.  
 XX

PF 09-APR-1999; 99WO-US007882.  
 XX  
 PR 10-APR-1998; 98US-00058660.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Donaldson D, Collins M, Whitters M, Neben T;  
 XX  
 DR WPI; 1999-611303/52.  
 DR N-PSDB; AAX90752.  
 XX  
 XX Novel polypeptides and polynucleotides used for treatment of human  
 PT diseases and disorders e.g. immune disorders or deficiencies caused by  
 PT fungal, parasitic or viral infections.  
 XX  
 XX Claim 9; Page 31-32; 43pp; English.  
 PS  
 XX The present sequence is a murine U4 protein which is a member of  
 CC haematopoietin receptor superfamily. The protein sequence has conserved  
 CC cysteine pairs and WSXS motifs characteristic of the receptor family. It  
 CC is predicted to have the following biological activities: cytokine, cell  
 CC proliferation/differentiation, immune stimulating or suppressing and  
 CC haematopoiesis regulating. The U4 protein can be used to treat immune  
 CC disorders and deficiencies, autoimmune disorders, allergies, cancer,  
 CC myeloid or lymphoid cell deficiencies and platelet disorders  
 XX  
 XX Sequence 425 AA;  
 SQ

Query Match 98.7%; Score 2225.5; DB 2; Length 425;  
 Best Local Similarity 98.6%; Pred. No. 7.8e-184; Indels 3; Gaps 1;  
 Matches 408; Conservative 2; Mismatches 1;

QY 1 MPAGRGPGVAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60  
 DB 1 MPAGRGPGVAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60  
 QY 61 ATCSIHGDTPGAETAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGAETAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYLRLW 180  
 DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYLRLW 180  
 QY 181 YGQDNTCEEVHTVGPHSCHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDP 240  
 DB 181 YGQDNTCEEVHTVGPHSCHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDP 240  
 QY 241 PPDVHVS RVGGLDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVDSNOTSCR 300  
 DB 241 PPDVHVS RVGGLDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVDSNOTSCR 300  
 QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGGVCEPRGGE 360  
 DB 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGGVCEPRGGE 360  
 QY 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
 DB 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 9  
 AAW70862  
 ID AAW70862 standard; protein; 425 AA.  
 XX  
 AC AAW70862;  
 XX  
 DT 17-MAR-1999 (first entry)  
 XX  
 XX Rat Zcytor5 protein.  
 DE  
 XX Zcytor5; cytokinin-like receptor; down-regulation; growth factor;  
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;  
 KW

KW cardiac pathology; heart enlargement; Zcytor5 ligand.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO9849307-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 01-MAY-1998; 98WO-US008865.  
 XX  
 PR 01-MAY-1997; 97US-0045287P.  
 PR 13-MAY-1997; 97US-00850030.  
 PR 13-FEB-1998; 98US-00023890.  
 PR 13-FEB-1998; 98US-0074721P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Lok S, Preenell SR, Jelmberg AC, Gilbert T, Whitmore TE;  
 PI Foster DC, Adams RL, Lehner JM;  
 XX  
 DR WPI; 1999-034662/03.  
 XX  
 XX N-PSDB; AAV70896.  
 XX  
 XX New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-  
 PT regulating Zcytor5 natural ligands or detecting cardiostrophin-1 in blood.  
 XX  
 XX Claim 1; Page 75-76; 55pp; English.  
 PS  
 XX The present sequence represents a protein designated Zcytor5, which is a  
 CC cytokinin-like receptor. Soluble Zcytor5 may be administered to down-  
 CC regulate the effects of a growth and/or maintenance factor in thyroid,  
 CC heart, and skeletal muscle for example to lessen the effect of  
 CC cardiostrophin-1 on cardiac pathologies, so preventing heart enlargement.  
 CC Zcytor5 could be used to detect cardiostrophin-1 in the blood, and to  
 CC discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA  
 CC or RNA can be used to determine the presence and integrity of the Zcytor5  
 CC gene on chromosome 19. Antibodies and the anti-idiotypic antibody could  
 CC be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand  
 CC effects  
 XX  
 SQ Sequence 425 AA;  
 Query Match 97.6%; Score 2197.5; DB 2; Length 425;  
 Best Local Similarity 97.6%; Pred. No. 1.1e-181; Indels 3; Gaps 1;  
 Matches 404; Conservative 3; Mismatches 4;

QY 1 MPAGRGPGVAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60  
 DB 1 MPAGRGPGVAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60  
 QY 61 ATCSIHGDTPGAETAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGAETAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYLRLW 180  
 DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYLRLW 180  
 QY 181 YGQDNTCEEVHTVGPHSCHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDP 240  
 DB 181 YGQDNTCEEVHTVGPHSCHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDP 240  
 QY 241 PPDVHVS RVGGLDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVDSNOTSCR 300  
 DB 241 PPDVHVS RVGGLDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVDSNOTSCR 300  
 QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGGVCEPRGGE 360  
 DB 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGGVCEPRGGE 360  
 QY 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
 DB 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 10  
 AAY29780  
 ID AAY29780 standard; protein; 416 AA.  
 XX  
 AC AAY29780;  
 XX  
 DT 04-NOV-1999 (first entry)  
 XX  
 DE Mouse DNAX soluble receptor subunit 1.  
 XX  
 KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 KW interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;  
 KW inflammatory disorder; inflammatory response; innate immunity;  
 KW morphogenic development; immunological disorder.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9940195-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 05-FEB-1999; 99WO-US002600.  
 XX  
 PR 06-FEB-1998; 98US-0073941P.  
 PR 13-MAY-1998; 98US-00078194.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Matteson JD, Mcclanahan TK, Kastelein RA;  
 XX  
 DR WPI; 1999-527306/44.  
 DR N-PSDB; AA208862.  
 XX  
 PT New receptor subunits useful in the treatment inflammatory disorders.  
 XX  
 PS Claim 2; Page 24-25; 133pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising DNAX  
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 CC subunit I (DSRS1) protein, which together encode a new mammalian cytokine  
 CC related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or  
 CC DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRS1 is useful for  
 CC screening for ligands (i.e. agonists/antagonists) from a library of  
 CC compounds, which are useful for modulating the physiology or development  
 CC of a cell or tissue culture e.g. inflammatory responses, innate immunity  
 CC and/or morphogenic development. (R), antibodies and ligands are useful  
 CC for treatment of conditions, especially immunological disorders,  
 CC associated with conditions exhibiting abnormal expression of (R). (R) is  
 CC useful as a phosphate labeling enzyme to label substrates, and the  
 CC subunits DSRs1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding  
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from  
 CC other individuals or species. The present sequence represents the  
 CC specifically claimed mouse DSRs1, for use in the composition of the  
 CC present invention  
 XX  
 SQ Sequence 416 AA;  
 Query Match 94.8%; Score 2134.5; DB 2; Length 416;  
 Best Local Similarity 98.7%; Pred. No. 3.3e-176;  
 Matches 392; Conservative 2; Mismatches 0; Indels 3; Gaps 1;  
 QY 18 RPLSLWSPLLCLVGVPRGSGANTAVISPODPTLLIGSSLOATCSIHGDPFGATAGL 77  
 DB 9 RPLSLWSPLLCLVGVPRGSGANTAVISPODPTLLIGSSLOATCSIHGDPFGATAGL 68  
 QY 78 YWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYVGLP 137  
 DB 69 YWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYVGLP 128  
 QY 138 PEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEYHTVGPHS 197

DB 129 PEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEYHTVGPHS 188  
 QY 198 CHIPKDLALFTPEIWEATNRLGARSDDLTLVDLVVTTTDPDPDVHVSRYGGLEDQLS 257  
 DB 189 CHIPKDLALFTPEIWEATNRLGARSDDLTLVDLVVTTTDPDPDVHVSRYGGLEDQLS 248  
 QY 258 VRWVSPALKKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCKLAGLKPGTVYFQVRCN 317  
 DB 249 VRWVSPALKKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCKLAGLKPGTVYFQVRCN 308  
 QY 318 PRGIYGSKAGIWSHSHPTAASRSPRPGCGGVCBPRGCGSPGVRRELKQFLGWL 377  
 DB 309 PRGIYGSKAGIWSHSHPTAASRSPRPGCGGVCBPRGCGSPGVRRELKQFLGWL 368  
 QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
 DB 369 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 405

RESULT 11  
 AAB19589  
 ID AAB19589 standard; protein; 407 AA.  
 XX  
 AC AAB19589;  
 XX  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE Mouse cytokine-like factor-1.  
 XX  
 KW Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; mouse; cytokine;  
 KW receptor; neuron; inflammation; anti-inflammatory; autoimmune disease;  
 KW therapy.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200053631-A1.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 09-MAR-2000; 2000WO-US0006182.  
 XX  
 PR 11-MAR-1999; 98US-00267901.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;  
 XX  
 DR WPI; 2000-587426/55.  
 XX  
 CC Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,  
 CC polypeptides, and nucleic acids, useful in research, diagnosis and for  
 CC treating inflammatory and autoimmune disorders.  
 XX  
 PS Claim 1; Page 21-22; 97pp; English.  
 CC  
 CC The present sequence is that of mouse cytokine-like factor-1 (CLF-1), a  
 CC cytokine receptor family protein, which forms a complex with human  
 CC interleukin-B60 (IL-B60, see AAB19586). The IL-B60/CLF-1 cytokine serves  
 CC as a key physiological factor in motor neuron development and  
 CC regeneration. A claimed soluble complex comprises at least 6 amino acids  
 CC of mature IL-60B, at least 6 amino acids of mature CLF-1 or at least 6  
 CC amino acids of mature CNTF-R. A claimed method of modulating the  
 CC physiology or development of a cell or tissue culture cell involves  
 CC contacting the cell with an agonist or antagonist of a complex comprising  
 CC IL-60B and CLF-1 or CNTF-R. A claimed method of screening for a receptor  
 CC which binds the complex involves contacting the complex with a cell  
 CC expressing the receptor, to form a detectable interaction resulting in a  
 CC physiological response in the cell  
 XX  
 SQ Sequence 407 AA;

Query Match 94.1%; Score 2119; DB 3; Length 407;

Best Local Similarity	98.5%;	Pred. No. 7e-175;			
Matches	391;	Conservative	2;	Mismatches	0;
		Indels	4;	Gaps	2
QY	18	RPLSLWSPLLLCVLGVPRGSGAHTAVISPDQPTLLIGSSLOATCSIHGDTFGATAEGL	77		
DB	1	RPLSLWSPLLLCVLGVPRGSGAHTAVISPDQPTLLIGSSLOATCSIHGDTFGATAEGL	60		
QY	78	YWTNGRRLPSLSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP	133		
DB	61	YWTNGRRLPS-LSELNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP	119		
QY	138	PEKPNISICWSGRNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQDNTCEEYHTVGPHS	197		
DB	120	PEKPNISICWSGRNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQDNTCEEYHTVGPHS	179		
QY	198	CHIPKDLALFTPYETIWEATNRLGASDVLTLDLVDVTTDPPDVHVSRYVGLEDQLS	257		
DB	180	CHIPKDLALFTPYETIWEATNRLGASDVLTLDLVDVTTDPPDVHVSRYVGLEDQLS	239		
QY	258	VWVWSPPALKDPLFOAKYQIRYRVEDSDVMKVDDVDSNOTSCRLAGLKPGCTVYFVQVRCN	317		
DB	240	VWVWSPPALKDPLFOAKYQIRYRVEDSDVMKVDDVDSNOTSCRLAGLKPGCTVYFVQVRCN	299		
QY	318	PFGIYGSKKAGIWSWSHPTAASTPRSERPGPGGVCEPRGSPGVVRRELKQPLGLWL	377		
DB	300	PFGIYGSKKAGIWSWSHPTAASTPRSERPGPGGVCEPRGSPGVVRRELKQPLGLWL	359		
QY	378	KKHAYCSNLSFRLYDQWRAWMQSHKHTNQ---VLPA	411		
DB	360	KKHAYCSNLSFRLYDQWRAWMQSHKHTNQDQEGILPS	396		

RESULT 12	
AAB36648	
ID	AAB36648 standard; protein; 407 AA.
XX	
AC	AAB36648;
XX	
DT	13-MAR-2001 (first entry)
XX	
XX	Mouse cytokine receptor subunit NR6 protein SEQ ID NO:5.
XX	
KW	DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW	modulating cell proliferation; diagnosis; detection; drug screening;
KW	immunological disorder.
XX	
OS	Mus sp.
XX	
PN	WO200073451-A1.
XX	
PD	07-DEC-2000.
XX	
XX	30-MAY-2000; 2000WO-US014867.
XX	
XX	01-JUN-1999; 99US-00322913.
XX	
PA	(SCHE ) SCHERING CORP.
XX	
PI	Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
XX	
XX	WPI; 2001-061536/07.
XX	
XX	Novel composition comprising DNAX cytokine receptor subunit polypeptide
PT	useful for regulating immune system function and for treating
PT	immunological disorders.
XX	
XX	Disclosure; Page 13-15; 93pp; English.
PS	
XX	
CC	The present invention describes a composition (I) comprising a
CC	recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The
CC	DCRS2 polypeptide is useful for binding ligands and for preparing
CC	antibodies. The DCRS2 polypeptide is also useful for modulating cell
CC	proliferation, for diagnostic and therapeutic applications, for detecting

CC presence of their ligands and in drug screening assays. It is also useful  
CC for treating conditions such as immunological disorders. The present  
CC sequence represents a cytokine receptor subunit protein, which is given in  
CC an alignment of various cytokine receptor subunits in the exemplification  
CC of the present invention  
XX  
XX Sequence 407 AA;  
SO

Query Match	94.1%; Score 2119; DB 4; Length 407;
Best Local Similarity	98.5%; Pred. No. 7e-175;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2	
QY	18 RPLSLWSPDLLLVLPVPRGSGAHTAVISPDQPTLLIGSSLQATCSIHGDTFGATAEGL 77
DB	1 RPLSLWSPDLLLVLPVPRGSGAHTAVISPDQPTLLIGSSLQATCSIHGDTFGATAEGL 60
QY	78 YWTLNGRLPSELGRLLNTSTLALANLNGSQOQGDNLVCHARDGSLIAGSCLVVGLP 137
DB	61 YWTLNGRLPSS-LSRLNTSTLALANLNGSRQOQGDNLVCHARDGSLIAGSCLVVGLP 119
QY	138 PEKPNISICWGRNMKDLTCRWTPCAHGETFLHTNYSLKYLRYWGQDNTCEEYHTVGPHS 197
DB	120 PEKPNISICWGRNMKDLTCRWTPCAHGETFLHTNYSLKYLRYWGQDNTCEEYHTVGPHS 179
QY	198 CHIPKDALFTPYEIWEATNRLGARS DVLTDVLVDVTTDPPDVHVS RVGGLEDQLS 257
DB	180 CHIPKDALFTPYEIWEATNRLGARS DVLTDVLVDVTTDPPDVHVS RVGGLEDQLS 239
QY	258 VFWVSPPALKDPLFOAKYQIHYRYVEDSDVMKVVDDVSNQTSCLAGLKPGTVTVFVQVRGN 317
DB	240 VFWVSPPALKDPLFOAKYQIHYRYVEDSDVMKVVDDVSNQTSCLAGLKPGTVTVFVQVRGN 299
QY	318 PFGIYGSKKAGIWSWSHPTAASPRSERPCGGGVCEPRGSGPVSRRRLKQFLGWL 377
DB	300 PFGIYGSKKAGIWSWSHPTAASPRSERPCGGGVCEPRGSGPVSRRRLKQFLGWL 359
QY	378 KGHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
DB	360 KGHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 396

RESULT 13	
ADC07180	
ID	ADC07180 standard; protein; 407 AA.
XX	
XX	
AC	ADC07180;
XX	
XX	
DT	18-DEC-2003 (first entry)
XX	
XX	
DE	Mouse cytokine receptor subunit NR7.
XX	
XX	
KW	DNAX cytokine receptor subunit 2; DCRS2; cell physiology;
KW	cell development; cell culture; interferon detection;
KW	immune system disorder; NR6; mouse.
KW	

OS	Mus sp.		
XX			
EN	US2003082734-A1.		
XX			
PD	01-MAY-2003.		
XX			
PF	18-SEP-2002; 2002US-00247463.		
XX			
PR	01-JUN-1999; 99US-0137159P.		
BR	31-MAY-2000; 2000US-00588113.		
XX			
FA	(DOWL/) DOWLING L M.		
PA	(TIMA/) TIMANS J C.		
PA	(GORM/) GORMAN D M.		
PA	(KAST/) KASTELEIN R A.		
PA	(BAZA/) BAZAN J F.		
XX			
PI	Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;		

XX WPI; 2003-730048/69.  
XX Composition potentially useful for treating immunological disorders,  
XX comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a  
PT natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2  
PT sequence.  
XX  
XX  
PS Disclosure; SEQ ID NO 5; 41pp; English.  
XX  
XX The invention describes a composition of matter (I) comprising a  
CC substantially pure or recombinant DNAX cytokine receptor subunit 2  
CC (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein  
CC comprising a DCRS2 sequence. A composition of matter comprises: a  
CC substantially pure or recombinant DCRS2 polypeptide comprising at least  
CC three distinct nonoverlapping segments of at least four amino acids  
CC identical to segments of a fully defined 384 amino acid sequence (S1),  
CC given in the specification; a substantially pure or recombinant DCRS2,  
CC polypeptide comprising at least two distinct nonoverlapping segments of  
CC at least five amino acids identical to segments of S1; a natural sequence  
CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.  
CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating  
CC physiology or development of a cell or cell culture. Antibodies to a  
CC DCRS2 can be used for quantitative detection of interferon. The DCRS2  
CC polypeptides and nucleic acids and their binding agents are potentially  
CC useful in treating and diagnosing disease, especially disease associated  
CC with the immune system. This is the amino acid sequence of mouse cytokine  
CC receptor subunit NR6 used in a comparison with DCRS2.  
XX  
XX Sequence 407 AA;

Query Match 94.1%; Score 2119; DB 7; Length 407;  
Best Local Similarity 98.5%; Pred. No. 7e-175; 0; Indels 4; Gaps 2;  
Matches 391; Conservative 2; Mismatches 2; Mismatches 0; Indels 4; Gaps 2;  
QY 18 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77  
DB 1 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60  
QY 78 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137  
DB 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119  
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEYHTVGP 197  
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEYHTVGP 179  
QY 198 CHIPKDALLFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 257  
DB 180 CHIPKDALLFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 239  
QY 258 VRWVSPALKDPLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKGTVYFVQVRCN 317  
DB 240 VRWVSPALKDPLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKGTVYFVQVRCN 299  
QY 318 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 377  
DB 300 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 359  
QY 378 KGHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
DB 360 KGHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 396

RESULT 14  
ADT90845  
ID ADT90845 standard; protein; 407 AA.  
XX  
XX ADT90845;  
XX  
XX 16-DEC-2004 (first entry)  
XX  
XX Mouse cytokine-like factor 1 (CLF-1).

XX Interleukin; IL-B60; cytokine-like factor 1; CLF-1; CNTF-R;  
KW CNTF-receptor; inflammatory condition; autoimmune disorder; mouse.  
XX  
XX Mus sp.  
XX  
XX US2004192891-A1.  
XX 30-SEP-2004.  
XX  
XX 11-FEB-2004; 2004US-00778002.  
XX  
XX 11-MAR-1999; 99US-0124319P.  
XX 09-MAR-2000; 2000US-00521335.  
XX (SCHE ) SCHERING CORP.  
XX  
XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;  
PI WPI; 2004-698788/68.  
XX GENBANK; NM\_004750.  
XX  
XX Novel mammalian cytokines, useful for producing antigen-antibody complex,  
PT treating conditions associated with abnormal physiology or development,  
PT including inflammatory conditions and/or autoimmune disorders.  
XX  
XX Claim 1; SEQ ID NO 13; 41pp; English.  
XX  
XX The invention relates to a complex comprising interleukin (IL)-B60,  
CC cytokine-like factor 1 (CLF-1) (partner sequence of IL-B60) and CNTF-R  
CC (CNTF-receptor). The complex is useful for producing an antigen-antibody  
CC complex, useful for treating conditions associated with abnormal  
CC physiology or development, including inflammatory conditions and/or  
CC autoimmune disorders and for generating antibodies which is useful in  
CC diagnostic applications. The present sequence is mouse cytokine-like  
CC factor 1 (CLF-1).  
XX  
XX Sequence 407 AA;

Query Match 94.1%; Score 2119; DB 8; Length 407;  
Best Local Similarity 98.5%; Pred. No. 7e-175; 0; Indels 4; Gaps 2;  
Matches 391; Conservative 2; Mismatches 2; Mismatches 0; Indels 4; Gaps 2;  
QY 18 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77  
DB 1 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60  
QY 78 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137  
DB 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119  
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEYHTVGP 197  
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEYHTVGP 179  
QY 198 CHIPKDALLFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 257  
DB 180 CHIPKDALLFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 239  
QY 258 VRWVSPALKDPLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKGTVYFVQVRCN 317  
DB 240 VRWVSPALKDPLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKGTVYFVQVRCN 299  
QY 318 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 377  
DB 300 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 359  
QY 378 KGHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
DB 360 KGHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 396

RESULT 15

ADT61033  
ID ADT61033 standard; protein; 407 AA.  
XX  
AC ADT61033;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
XX Mouse cytokine-like factor 1 (CLF-1).  
DE  
XX Cytokine; interleukin-B60; IL-B60; cell physiology; immune system;  
KW haematopoietic cell; immune disorder; T cell immune deficiency;  
KW chronic inflammation; tissue rejection; cardiovascular condition;  
KW neurophysiological condition; mouse; cytokine-like factor 1; CLF-1.  
XX  
OS Mus sp.  
XX  
PN US6800460-B1.  
XX  
XX  
PD 05-OCT-2004.  
XX  
XX 09-MAR-2000; 2000US-00521335.  
XX  
PR 11-MAR-1999; 99US-0124319P.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;  
PI WPI; 2004-697202/68.  
XX  
DR New isolated or non-human host cells transfected with expression vectors  
XX having nucleic acids encoding cytokines, useful in treating immune  
PT disorders, cardiovascular or neurophysiological conditions.  
XX  
XX Disclosure; SEQ ID NO 13; 37pp; English.  
XX  
XX The invention relates to mammalian interleukin-B60 (IL-B60). The  
CC invention also provides a method of producing a soluble complex  
CC comprising the mature protein portions of IL-B60 and CLF-1 polypeptides.  
CC The methods and compositions of the present invention are useful in  
CC controlling biology and physiology of mammalian cells, such as cells of a  
CC mammalian immune system, and in particular for regulating activation,  
CC development, differentiation and function of various cell types,  
CC including haematopoietic cells. They are specifically useful in treating  
CC abnormal medical conditions, including immune disorders, such as T cell  
CC immune deficiency, chronic inflammation or tissue rejection, or in  
CC cardiovascular or neurophysiological conditions. The present sequence is  
CC the mouse cytokine-like factor 1 (CLF-1).  
XX  
XX Sequence 407 AA;

Query Match 94.1%; Score 2119; DB 8; Length 407;  
Best Local Similarity 98.5%; Pred. No. 7e-175;  
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY	18	RPLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTFCATAEGL	77
DB	1	RPLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTFCATAEGL	60
QY	78	YWTINGRRRLPSELRLINTSTLALANLNGSQSGDNLVCHARDGSILAGSCLYGLP	137
DB	61	YWTINGRRRLPS-LSRLINTSTLALANLNGSQSGDNLVCHARDGSILAGSCLYGLP	119
QY	138	PEKPFNISCWRNWKDITCRWTPGAGHGETFLHNTNYSKYLKWYGQDNTCEEYHTVGPHS	197
DB	120	PEKPFNISCWRNWKDITCRWTPGAGHGETFLHNTNYSKYLKWYGQDNTCEEYHTVGPHS	179
QY	198	CHIPKOLALFTPYEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVS RVGGLDQLS	257
DB	180	CHIPKOLALFTPYEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVS RVGGLDQLS	239
QY	258	VRWVSPPALXDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAGLKGTVVFQVRCN	317

Db 240 VRWVSPPALXDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAGLKGTVVFQVRCN 299  
QY 318 PFGIYGSKKAGIWSWSHPTAASTPRSRPGRPGGVCEPRGGEPSGVPVRELKQFLGWL 377  
Db 300 PFGIYGSKKAGIWSWSHPTAASTPRSRPGRPGGVCEPRGGEPSGVPVRELKQFLGWL 359  
QY 378 KKHAYCSNLSFELYDOWBAWMOKSHKTRNQ---VLPA 411  
Db 360 KKHAYCSNLSFELYDOWBAWMOKSHKTRNQDEGILPS 396

Search completed: April 11, 2006, 02:09:56  
Job time : 113.845 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	331	14.7	288	2	B59405	prolactin receptor
2	331	14.7	376	2	A59405	prolactin receptor
3	331	14.7	622	2	A40144	prolactin receptor
4	329	14.6	918	2	A36337	membrane glycoprot
5	319.5	14.2	917	2	I49699	glycoprotein 130 -
6	317.5	14.1	918	2	A44257	interleukin-6 sign
7	314	13.9	830	2	I50455	prolactin receptor
8	312	13.9	310	2	A29884	prolactin receptor
9	312	13.9	610	2	A41070	prolactin receptor
10	312	13.9	610	2	A34631	lactogen receptor
11	312	13.9	610	2	A36116	prolactin receptor
12	307.5	13.7	292	2	I77525	prolactin receptor
13	307.5	13.7	303	2	I77524	prolactin receptor
14	307.5	13.7	608	2	I52269	prolactin receptor
15	307.5	13.7	616	2	A30304	prolactin receptor
16	306	13.6	831	2	IQ1655	prolactin receptor
17	302.5	13.4	581	2	I45971	prolactin receptor
18	261.5	11.6	630	2	I51086	prolactin receptor
19	254.5	11.3	771	2	B39252	granulocyte colony
20	254.5	11.3	783	2	JH0329	granulocyte colony
21	254.5	11.3	863	2	C38252	granulocyte colony
22	252.5	11.2	837	2	A34898	granulocyte colony
23	234	10.4	372	2	I58141	ciliary neurotroph
24	220.5	9.8	372	1	UHHUCN	ciliary neurotroph
25	209.5	9.3	422	2	I37891	interleukin-11 rec
26	208.5	9.3	432	2	I48343	interleukin-11 rec
27	208	9.2	362	2	S60614	growth promoting a
28	203.5	9.0	460	2	JL0145	interleukin-6 rece
29	200.5	8.9	468	1	A41242	interleukin-6 rece

126	Qy	ILAGSCLYVG-LPPEKFPNISCWGRNMKDLTCRWTPGAGHETFLTNTVSLKYKLRYGQD	184
15	Db	LFLNTLLINGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNLSLYHREGETILM	72
185	Qy	NTCEEYHVGPHSCHI PKD-LALPTPYEIWYEAATNRLGASASDVLTLVDLVVYTTDPPD	243
73	Db	HECPDYITGGNSCHFGKQYTSWRTYIMVYNATNQMGSPSDESLVDVYTVQDPDPLE	132
244	Qy	VHYSRVGLEDOLSVRWV--SPPALKDF--LFAQYQIRYRVEDSVDMKVDDVDSNQT	298
133	Db	LAV-EVKQPEDRKPYLMIKWSPPFLIDUKTGWFTLLYIRUKPEKAAEWE-IHFAGQQTE	190
299	Qy	CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTP	342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 2

A59405

prolactin receptor short form Sla precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

C:Accession: A59405

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin receptor

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: A59405

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU>

A:Cross-references: UNIPROT:Q96P35; UNIPARC:UPI000006E673; GB:AF214012.1

R:Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: A49400

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU>

A:Cross-references: UNIPARC:UPI000006E673; GB:AF214012.1

C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor

eta-casein gene promoter activation, with S1a less effective than S1b. However, their li

ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: Sp13.3-Sp13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 331; DB 2; Length 376;

Best Local Similarity 37.5%; Pred. No. 3.7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLYVG-LPPEKPFNISCWSRNKDLTCRWTFGAHGETFLHTNYSLKYLKRWYQD 184

Db 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLYTHREGETLM 72

QY 185 NTCEEYHTVGPCHSCHKPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPPPD 243

Db 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQSGSFSDLYVDVTYIVQDPDPLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVDSVDMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRPYLVWIKWSPPTLIDLTGWTFLYELRLKPEKAAWE-IHFAGQOTE 190

QY 299 CRLAGLKPQTVYFVQRCNPFYIGSKKAGINSEWSHPTAASTP 342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

Query Match 14.7%; Score 331; DB 2; Length 376;

Best Local Similarity 37.5%; Pred. No. 3.7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLYVG-LPPEKPFNISCWSRNKDLTCRWTFGAHGETFLHTNYSLKYLKRWYQD 184

Db 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLYTHREGETLM 72

QY 185 NTCEEYHTVGPCHSCHKPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPPPD 243

Db 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQSGSFSDLYVDVTYIVQDPDPLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVDSVDMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRPYLVWIKWSPPTLIDLTGWTFLYELRLKPEKAAWE-IHFAGQOTE 190

QY 299 CRLAGLKPQTVYFVQRCNPFYIGSKKAGINSEWSHPTAASTP 342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 3

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

C:Accession: A40144; A57018

R:Boutin, J.M.; Edery, M.; Shiota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.;

Mol. Endocrinol. 3, 1455-1461, 1989

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human he

A:Reference number: A40144; MUID:90114212; PMID:2558309

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BOU>

A:Cross-references: UNIPROT:P16471; UNIPARC:UPI0000132234; GB:M31661; NID:G190361; PIDN:

R:Fuh, G.; Wells, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li

A:Reference number: A57018; MUID:95286597; PMID:7768908

A:Accession: A57018

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 25-228, 'AW' <RES>

A:Cross-references: UNIPARC:UPI000006D208; GB:S78505; NID:G999114; PIDN:AAB34470.1; PID:

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: Sp13.3-Sp13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-622/Product: prolactin receptor, long form #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 331; DB 2; Length 622;

Best Local Similarity 37.5%; Pred. No. 7.1e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLYVG-LPPEKPFNISCWSRNKDLTCRWTFGAHGETFLHTNYSLKYLKRWYQD 184

Db 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLYTHREGETLM 72

QY 185 NTCEEYHTVGPCHSCHKPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPPPD 243

Db 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQSGSFSDLYVDVTYIVQDPDPLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVDSVDMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRPYLVWIKWSPPTLIDLTGWTFLYELRLKPEKAAWE-IHFAGQOTE 190

QY 299 CRLAGLKPQTVYFVQRCNPFYIGSKKAGINSEWSHPTAASTP 342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 4

A36337

membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C>Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004

C:Accession: A36337

R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MUID:91084844; PMID:2261637

A:Accession: A36337

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: UNIPROT:P40189; UNIPARC:UPI0000046B12; GB:M57230; NID:G186353; PIDN:

C:Genetics:

A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694

A:Map position: 5q11-5q11

C:Keywords: glycoprotein; membrane protein

F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 14.6%; Score 329; DB 2; Length 918;

Best Local Similarity 28.6%; Pred. No. 1.6e-17;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPDPTLIGSSLQATCSIHG---DTPGATAGLWTLNRLPSELRLNTSTLALA 102

Db 31 ISPESPVQLHSNFTAVCVLKERCMDFYHNANYIVKTNHFTIPKEQYTIINRTASSVT 90

QY 103 LANLNGSRQSGDNLVCHARDGSLAGSLYGLPPEKPFNISCWSRNKDLTCRWTPGA 162

```
Db 91 FTDIASLNLTGTCNLTITGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMCEWDGGR 150
QY 163 HGETFLHTNYSKYLKWYQODNTCEYHTVGVPHSGHIPKDLALFTPYEITWEATNRLGS 222
Db 151 --ETHLETNFTLASEWATHKFAACKAKRDT--PTSCVDYSTVYFVNIWVEAENALGK 206
QY 223 ARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKPLFOAKYQIRYRV 282
Db 207 VTSDHINFDPVYKVPKPNHLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK 264
QY 283 DSDVMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPNPGIYSGKAGIWSWSHPTAA 339
Db 265 DASTWQIPEPTASTRSSFTVQDLKPFTYEVFRIR-----WKEDGKGWSDWSEASG 319
QY 340 STPRSERP 347
Db 320 IT-YEDRP 326

RESULT 5
I49699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:92291532; PMID:1602143
A:Accession: I49699
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPROT:Q00560; UNIPARC:UPI000002845A; GB:M83336; NID:G193591; PIDN:
A:Accession: I48370
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:G840816; PIDN:CAA44515.1; PI
C:Genetics:
A:Gene: gp130
C:Keywords: Glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 14.2%; Score 319.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 9e-17;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPDPTLLIGSSLOATCSIHG---DTPGATAGLYWTILNGRRRLPSELRLNTSTLALA 102
Db 31 IYPEPPVQVQSGNFTATCVLKEACLOHYVYNASYIWKTNHAAVPEQVTVINRTTSSVT 90
QY 103 LANLNGRQSGDNLVCHARDGSIAGSCLYGLPPEKPFNISCWRNNKMDLTCRWTPGA 162
Db 91 FTDVVLPSVQLTCNLLISFGQIEQNVYGVMTLSGFFPKPTNLTCIVNEGKNMLCQWDPCR 150
QY 163 HGETFLHTNYSKYLKWYQOD-NTCEEYHTVGVPHSGHIPKDLALFTPYEITWEATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDCCQKHGT---SCMVSYMTPTYYVNIWVEAENALG 203
QY 222 SARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKPLFOAKYQIRYRV 281
Db 204 KYVSESINFDPVDVKVPTPPNLSVNTSELSILKLSVSSGL--GGILLDKSDIQYRT 261
QY 282 EDSVDMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPNPGIYSGKAGIWSWSHPTA 338
Db 262 KDASTWQIPELDTMSPTSTFTVQDLKPFTYEVFRIR-----SIKSGK-GYNSDWSEAS 316
QY 339 AST--PRSERP 347
Db 317 GTTYEDRPSRP 327

Query Match 14.2%; Score 319.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 9e-17;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPDPTLLIGSSLOATCSIHG---DTPGATAGLYWTILNGRRRLPSELRLNTSTLALA 102
Db 31 IYPEPPVQVQSGNFTATCVLKEACLOHYVYNASYIWKTNHAAVPEQVTVINRTTSSVT 90
QY 103 LANLNGRQSGDNLVCHARDGSIAGSCLYGLPPEKPFNISCWRNNKMDLTCRWTPGA 162
Db 91 FTDVVLPSVQLTCNLLISFGQIEQNVYGVMTLSGFFPKPTNLTCIVNEGKNMLCQWDPCR 150
QY 163 HGETFLHTNYSKYLKWYQOD-NTCEEYHTVGVPHSGHIPKDLALFTPYEITWEATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDCCQKHGT---SCMVSYMTPTYYVNIWVEAENALG 203
QY 222 SARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKPLFOAKYQIRYRV 281
Db 204 KYVSESINFDPVDVKVPTPPNLSVNTSELSILKLSVSSGL--GGILLDKSDIQYRT 261
QY 282 EDSVDMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPNPGIYSGKAGIWSWSHPTA 338
Db 262 KDASTWQIPELDTMSPTSTFTVQDLKPFTYEVFRIR-----SIKSGK-GYNSDWSEAS 316
QY 339 AST--PRSERP 347
Db 317 GTTYEDRPSRP 327
```

## RESULT 6

```
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R;Wang, Y.; Nesbitt, J.B.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257; MUID:93052397; PMID:1427893
A:Accession: A44257
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBI:P118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>
```

```
Query Match 14.1%; Score 317.5; DB 2; Length 918;
Best Local Similarity 29.8%; Pred. No. 1.3e-16;
Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;
```

```
QY 46 ISPDPTLLIGSSLOATCSIHG---DTPGATAGLYWTILNGRRRLPSELRLNTSTLALA 102
Db 31 IYPEPPVQVQSGNFTATCVLKECLQVYSVNATYIWKTNHVAVPKEQVTVINRTASSVT 90
QY 103 LANLNGRQSGDNLVCHARDGSIAGSCLYGLPPEKPFNISCWRNNKMDLTCRWTPGA 162
Db 91 FTDVVFQNVQLTCNLLISFGQIEQNVYGITILSGYDPIPTNLSCIVNEGKNMLCQDPCR 150
QY 163 HGETFLHTNYSKYLKWYQOD-NTCEEYHTVGVPHSGHIPKDLALFTPYEITWEATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDCCRTKH--GTSSCMGMYPTIYVNIWVEAENALG 204
QY 222 SARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKPLFOAKYQIRYRV 281
Db 205 NVYSEPIINFDPVDVKVPPHNLSTVNTSELSILKLAWNVSL--DSILRLKSDIQYRT 262
QY 282 EDSVDMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPNPGIYSGKAGIWSWSHPTA 338
Db 263 KDASTWQIPELDTVSPRTSFTVQDLKPFTYEVFRIR-----SIKENGK-GYNSDWSE-EA 316
QY 339 ASTPRSERP 347
Db 317 SGTTYEDRP 325
```

## RESULT 7

```
I50455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R;Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267; PMID:7516866
A:Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:G466381; PI
F:36-220/Domain: cytokine receptor homology <CRS>
F:240-426/Domain: cytokine receptor homology <CRS>
```

```
Query Match 13.9%; Score 314; DB 2; Length 830;
Best Local Similarity 37.1%; Pred. No. 2.1e-16;
Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PPEKPFNISCWRNNKMDLTCRWTPGAHGTFLH-TNYSILKYLKWYQDNTCEYHTVGP 195
```



Db 206 ----DHGYWSRWGQEKSIETP 222

RESULT 13

177524

prolactin receptor precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C:Accession: I77524

R:Davis, J.A.; Linzer, D.I.H.

Mol: Endocrinol. 3, 674-680, 1989

A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.

A:Reference number: I57699; MUID:89261824; PMID:2725531

A:Accession: I77524

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-303 <RES>

A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B197; GB:M22958; NID:g200479; PIDN:F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 307.5; DB 2; Length 303;

Best Local Similarity 32.6%; Pred. No. 1.9e-16;

Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

Qy 90 LSRLLNTSTLALANLANLSRQSGDNLVCHARDGSIILAGSLYVGLPPEKPFNISCWSR 149

Db 1 MSSALAYMLLVLSISLLNG---QS-----PPGKEIHKCRSP 34

Qy 150 NMKDLTCRWTFGANGETFLHTNYSIKYKLRWGYQDNT--CBEYHTVGPHSCHIPKD-LAL 206

Db 35 DKETFTCWNPFGSDGG--LPTNYSILYTSKE--GEKNITYECDYKTSGPNSCFFSKQYTSI 90

Qy 207 FTPPEIWEATNRLGARSARDVLTLDLVDVTTDPPDVHVSRVGGLDQLSVRWVS--pp 264

Db 91 WKYIIITVATNMGSTSDSLYVDVTVIVPEPPRNUTL-EVKQLKOKKTYLWVKWLPP 149

Qy 265 ALKDF---LFOAKYQIRYRVEDSVDMKVVDVDSNCTSLRAGLKPGETVYFVQVRGNPFGI 321

Db 150 TITDVKTGWFTMEYELRLKSEADEWE-IHTFGHTQFKVPDLYPGQKYLVTQRCKP--- 205

Qy 322 YGSKKAGIWSWSHPTAASTP 342

Db 206 ----DHGYWSRWGQEKSIETP 222

RESULT 14

153269

prolactin receptor, long form - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C:Accession: I53269; JT0671; S34356

R:Clarke, D.L.; Linzer, D.I.H.

Endocrinology 133, 224-232, 1993

A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.

A:Reference number: I53269; MUID:93307149; PMID:8319571

A:Accession: I53269

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-608 <RES>

A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:L14811; NID:g293769; PIDN:R;Moore, R.C.; Oka, T.

Gene 134, 263-265, 1993

A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form

A:Reference number: JT0671; MUID:94085788; PMID:8262385

A:Accession: JT0671

A:Molecule type: mRNA

A:Residues: 1-608 <MOO>

A:Cross-references: UNIPARC:UPI0000020E90; GB:L13593; NID:g347398; PIDN:R;Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.

submitted to the EMBL Data Library, June 1993

A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.

A:Reference number: S34356



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:04:23 ; Search time 123.014 Seconds  
(without alignments)  
2368.694 Million cell updates/sec

Title: US-09-037-657-13

Perfect score: 2251

Sequence: 1 MPAGRPGVQAQRPRPL.....WRANQKSHKTRNQVLPKAL 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_05.80.\*

1: uniprot\_spport.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2226.5	98.9	425	1 CR1F1_MOUSE	Q9Jm58 mus musculus
2	2096	93.1	422	1 CR1F1_HUMAN	O75462 homo sapien
3	1422.5	63.2	389	2 Q6DG28_BRARE	O6dg28 brachydanio
4	1382.5	61.4	394	2 Q6UA05_TETNG	O6uaq5 tetraodon n
5	995	44.2	437	2 Q4RMP5_TETNG	Q4rmp5 tetraodon n
6	468.5	20.8	207	2 Q4TCM7_TETNG	Q4tcm7 tetraodon n
7	416	18.5	151	2 Q4RDR1_TETNG	Q4rdr1 tetraodon n
8	380	16.9	199	2 Q4RDQ9_TETNG	Q4rdq9 tetraodon n
9	371	16.5	918	2 Q9W6U9_CHICK	Q9w6u9 gallus gall
10	355.5	15.8	881	2 O57519_XENLA	O57519 xenopus lae
11	332	14.7	268	2 Q8CD78_HUMAN	Q8cd78 homo sapien
12	331	14.7	288	2 Q96P36_HUMAN	Q96p36 homo sapien
13	331	14.7	349	2 Q9UHJ5_HUMAN	Q9uhj5 homo sapien
14	331	14.7	376	2 Q96P35_HUMAN	Q96p35 homo sapien
15	331	14.7	622	1 PRLR_HUMAN	P16471 homo sapien
16	331	14.7	622	2 Q5RAW0_PONPY	Q5raw0 pongo pygma
17	330.5	14.7	1010	2 Q77Q89_RAT	Q77q89 rattus norv
18	329	14.6	857	2 Q5FC04_HUMAN	Q5fc04 homo sapien
19	329	14.6	918	1 ILGRB_HUMAN	P40189 homo sapien
20	319.5	14.2	917	1 ILGRB_MOUSE	Q00560 mus musculus
21	319.5	14.2	917	2 Q6PD19_MOUSE	Q6pd19 mus musculus
22	317.5	14.1	918	1 ILGRB_RAT	P40190 rattus norv
23	316	14.0	622	2 Q9N0J7_CALJA	Q9n0j7 callithrix
24	314.5	14.0	608	2 Q99JZ1_MOUSE	Q99jz1 mus musculus
25	314	13.9	622	2 Q865V4_CEBAP	Q865v4 cebus apell
26	314	13.9	830	1 PRLR_COLLI	Q90374 columba liv
27	312	13.9	310	2 Q58DZ7_RAT	Q58dz7 rattus norv
28	312	13.9	610	1 PRLR_RAT	P05710 rattus norv
29	307.5	13.7	292	2 Q8C7G1_MOUSE	Q8c7g1 mus musculus
30	307.5	13.7	608	1 PRLR_MOUSE	Q08501 mus musculus
31	307.5	13.7	616	1 PRLR_RABIT	P14787 oryctolagus

32	307	13.6	625	1 PRLR_PIG	Q6jta8 sus scrofa
33	306	13.6	460	2 Q7T2Z0_CHICK	Q7t2z0 gallus gall
34	306	13.6	581	1 PRLR_SHEEP	O46561 ovis aries
35	306	13.6	831	1 PRLR_CHICK	O04594 gallus gall
36	306	13.6	831	2 Q6QDA0_CHICK	Q6qda0 gallus gall
37	305	13.5	831	1 PRLR_MELGA	Q91094 meleagris g
38	303	13.5	581	1 PRLR_CEREL	Q28235 cervus elap
39	302.5	13.4	581	1 PRLR_BOVIN	Q28172 bos taurus
40	294	13.1	611	2 Q9PTH9_XENLA	Q9pth9 xenopus lae
41	289.5	12.9	604	2 Q6UAP8_TETNG	Q6uap8 tetraodon n
42	289	12.8	357	2 Q4SQD8_TETNG	Q4sqd8 tetraodon n
43	289	12.8	819	2 Q616F7_EUMA	Q616f7 eublepharis
44	288.5	12.8	611	2 Q91BF6_XENLA	Q91bf6 xenopus lae
45	288.5	12.8	611	2 Q9PTI0_XENLA	Q9pti0 xenopus lae

#### ALIGNMENTS

RESULT 1	ID	CR1F1_MOUSE	STANDARD;	PRT;	425 AA.
AC	Q9Jm58;				
DT	29-MAR-2004 (Rel. 43, Created)				
DT	29-MAR-2004 (Rel. 43, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)				
DE	(CLF-1) (Cytokine receptor-like molecule 3) (CRLM-3) (NR6).				
GN	Name=Crlf1; Synonyms=Crlm3;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muroidea; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1] NUCLEOTIDE SEQUENCE.				
RP	Hiroyana T., Iwana A., Nakamura Y., Nakauchi H.;				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	FUNCTION, AND TISSUE SPECIFICITY.				
RX	PubMed10359701; DOI=10.1016/S0960-9822(99)80266-8;				
RA	Alexander W.S., Raker S., Robb L., Farley A., Willson T.A.,				
RA	Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,				
RA	Hasegawa M., Maeda M., Fabri L., Jachno K., Nash A., Metcalf D.,				
RT	Nicola N.A., Hilton D.J.;				
RT	"Suckling defect in mice lacking the soluble haemopoietin receptor				
RL	NR6.";				
RL	Curr. Biol. 9:605-608 (1999).				
RN	[3]				
RP	PHOSPHORYLATION SITE SER-222.				
RX	PubMed15378723; DOI=10.1002/tcm.1604;				
RA	Jin W.-H., Dai J., Zhou H., Xia Q.-C., Zou H.-F., Zeng R.;				
RT	"Phosphoproteome analysis of mouse liver using immobilized metal				
RT	affinity purification and linear ion trap mass spectrometry.";				
RL	Rapid Commun. Mass Spectrom. 18:2169-2176 (2004).				
CC	!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory				
CC	role in the immune system and during fetal development. May be				
CC	involved in nervous system development (By similarity). Plays an				
CC	essential role in the initiation and/or maintenance of suckling in				
CC	neonatal mice.				
CC	!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a				
CC	heteromeric complex with cardiotrophin-like cytokine (CLC); the				
CC	CRF1/CLC complex is a ligand for the ciliary neurotrophic factor				
CC	receptor (CNTFR) (By similarity).				
CC	!- SUBCELLULAR LOCATION: Secreted (By similarity).				
CC	!- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected				
CC	in the brain of adult mice.				
CC	!- DOMAIN: The WSXWS motif appears to be necessary for proper protein				
CC	folding and thereby efficient intracellular transport and cell-				
CC	surface receptor binding.				
CC	!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3				
CC	subfamily.				
CC	!- SIMILARITY: Contains 2 fibronectin type-III domains.				

CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
CC domain.

CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC -----  
CC EMBL: AB040038; BAA92777.1; -; mRNA.  
CC HSSP: PA0223; 1CD9.  
CC Ensembl: ENSMUSG0000007888; Mus musculus.  
CC MGI: MGI:1340030; Crfl1.  
CC GO: GO:0005615; C:extracellular space; TAS.  
CC InterPro: IPR002996; Cytokn recept\_B/G.  
CC InterPro: IPR003961; FN III  
CC InterPro: IPR007110; Ig-like.  
CC Pfam: PF00041; fn3; 2.  
CC SMART: SM00060; FN3; 2.  
CC PROSITE: PS50853; FN3; 2.  
CC PROSITE: PS50835; IG LIKE; FALSE NEG.  
CC Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;  
KW Repeat; Signal.  
FT SIGNAL 1 33 Potential.  
FT CHAIN 34 425 Cytokine receptor-like factor 1.  
FT DOMAIN 35 134 Ig-like C2-type.  
FT DOMAIN 137 232 Fibronectin type-III 1.  
FT DOMAIN 237 337 Fibronectin type-III 2.  
FT MOTIF 330 334 WXSWS motif.  
FT MOD\_RES 222 222 Phosphoserine.  
FT CARBOHYD 95 95 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 107 107 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 143 143 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 171 171 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 295 295 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 385 385 N-linked (GlcNAc. .) (Potential).  
FT DISULFID 146 156 By similarity.  
FT DISULFID 187 198 By similarity.  
FT SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 98.9%; Score 2226.5; DB 1; Length 425;  
Best Local Similarity 98.8%; Pred. No. 1.8e-168;  
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;  
  
QY 1 MPAGRGPVQAQARRPRPLSSLSWSPLLLCVLGVRGGSGAHTAVISPDPTLLIGSSLQ 60  
DB 1 MPAGRGPVQAQARRPRPLSSLSWSPLLLCVLGVRGGSGAHTAVISPDPTLLIGSSLQ 60  
  
QY 61 ATCSIHGDTFGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 61 ATCSIHGDTFGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
  
QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNMKDLTCRWTPGAGETFLHTNYSCLKLRW 180  
DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNMKDLTCRWTPGAGETFLHTNYSCLKLRW 180  
  
QY 181 YGQDNTECEVHTVGRHSCHLPKDALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240  
DB 181 YGQDNTECEVHTVGRHSCHLPKDALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240  
  
QY 241 PPDVHVSRVGGLDQLSVRVSPALPKDFLQAKYQIRYRVDSVDMKWVDDVSNQTSR 300  
DB 241 PPDVHVSRVGGLDQLSVRVSPALPKDFLQAKYQIRYRVDSVDMKWVDDVSNQTSR 300  
  
QY 301 LAGLKPCTVTVQVRCNPFYIGSKAGIWSHSHPTAASPRSRPGGGVCEPRGGE 360  
DB 301 LAGLKPCTVTVQVRCNPFYIGSKAGIWSHSHPTAASPRSRPGGGVCEPRGGE 360  
  
QY 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQRAWWQKSHKTRNQ---VLPA 411  
DB 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQRAWWQKSHKTRNQDEGILPS 414

RESULT 2  
CRLF1 HUMAN STANDARD; PRT; 422 AA.  
ID AC Q75462; Q9UHH5;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)  
DE (CLF-1) (Zcytor5).  
GN Name=CRLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
RN NCBI\_TaxID=9606;  
RX MEDLINE=98349389; PubMed=9686600;  
RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,  
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;  
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with  
RT members of the cytokine type I receptor family.";  
RT J. Immunol. 161:1371-1379(1998).  
RL [1]  
RP NUCLEOTIDE SEQUENCE, SUBUNIT, SUBCELLULAR LOCATION, TISSUE  
RP SPECIFICITY, AND INDUCTION.  
RC TISSUE=Fetal lung;  
RX MEDLINE=98349389; PubMed=9686600;  
RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,  
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;  
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with  
RT members of the cytokine type I receptor family.";  
RT J. Immunol. 161:1371-1379(1998).  
RL [2]  
RN NUCLEOTIDE SEQUENCE.  
RA Magrangeas F., Jacques Y., Minvielle S.;  
RT "Cloning and expression of a novel soluble protein containing  
RT hemopoietic cytokine receptor domains";  
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RL [3]  
RN NUCLEOTIDE SEQUENCE.  
RA Lok S., Presnell S.R., Jellmberg A.C., Gilbert T., Whitmore T.E.,  
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;  
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RL [4]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,  
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RT Genome Res. 13:2265-2270(2003).  
RL [5]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley A.C., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez R.C., Gough J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP [6]  
 RX PROTEIN SEQUENCE OF 38-52  
 RA PubMed:15340161; DOI=10.1101/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RA "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [7]  
 RP INTERACTIONS WITH CLC AND CNTRP.  
 RX MEDLINE=20423191; PubMed=10966616; DOI=10.1038/78765;  
 RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H.,  
 RA Froger J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y.,  
 RA Gauchat J.-F., Gascan H.;  
 RA "CLF associates with CLC to form a functional heteromeric ligand for  
 RT the CNTRP receptor complex.";  
 RL Nat. Neurosci. 3:867-872(2000).  
 RN [8]  
 RP VARIANTS CISS HIS-81 AND ARG-374.  
 RX MEDLINE=22428294; PubMed=12509788;  
 RA Knappskog P.M., Majewski J., Livneh A., Nilsson P.T.E., Bringsli J.S.,  
 RA Ott J., Boman H.;  
 RA "Cold-induced sweating syndrome is caused by mutations in the CRLF1  
 RT gene.";  
 RL Am. J. Hum. Genet. 72:375-383(2003).  
 CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory  
 CC role in the immune system and during fetal development. May be  
 CC involved in nervous system development.  
 CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a  
 CC heteromeric complex with cardiotrophin-like cytokine (CLC); the  
 CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor  
 CC receptor (CNTRP).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Highest levels of expression observed in  
 CC spleen, thymus, lymph node, appendix, bone marrow, stomach,  
 CC placenta, heart, thyroid and ovary. Strongly expressed also in  
 CC fetal lung.  
 CC -!- INDUCTION: Up-regulated in fibroblast primary cell cultures under  
 CC stimulation by IPN-gamma, TNF-alpha and IL-6.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding.  
 CC -!- DISEASE: Defects in CRLF1 are the cause of cold-induced sweating  
 CC syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive  
 CC disorder characterized by profuse sweating induced by cool  
 CC surroundings (temperatures of 7 to 18 degrees Celsius). Additional  
 CC abnormalities include a high-arched palate, nasal voice, depressed  
 CC nasal bridge, inability to fully extend the elbows and  
 CC kyphoscoliosis.  
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
 CC domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AF059293; AAC38335.1; -; mRNA.  
 CC EMBL; AF073515; AAD39681.1; -; mRNA.  
 CC EMBL; AF178684; AAD54385.1; -; mRNA.  
 CC EMBL; AY358291; AAQ88658.1; -; mRNA.  
 CC EMBL; BC044634; AAH44634.1; -; mRNA.  
 CC HSP; P40223; 1CD9.  
 CC Ensembl; ENSG00000006016; Homo sapiens.  
 CC HGNC; HGNC:2364; CRLF1.  
 CC MIM; 604237; -.  
 CC MIM; 272430; -.

DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0019955; F:cytokine binding; IPI.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0019735; F:antimicrobial humoral response (sensu Verte. . . ; TAS.  
 DR InterPro; IPR002996; C:cytokine\_recept\_B/G.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00041; fn3; 2.  
 DR PROSITE; PS50853; FN3; 2.  
 DR PROSITE; PS50835; IG LIKE; FALSE\_NEG.  
 KW Direct protein sequencing; Disease mutation; Glycoprotein;  
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.  
 FT SIGNAL 1 37  
 FT CHAIN 38 422 Cytokine receptor-like factor 1.  
 FT DOMAIN 38 131 Ig-like C2-type.  
 FT DOMAIN 134 229 Fibronectin type-III 1.  
 FT DOMAIN 234 334 Fibronectin type-III 2.  
 FT MOTIF 327 331 WSXWS motif.  
 FT MOD\_RES 219 219 Phosphoserine (By similarity).  
 FT CARBOHYD 92 92 N-linked (GlcNAc. . . ) (Potential).  
 FT CARBOHYD 104 104 N-linked (GlcNAc. . . ) (Potential).  
 FT CARBOHYD 140 140 N-linked (GlcNAc. . . ) (Potential).  
 FT CARBOHYD 168 168 N-linked (GlcNAc. . . ) (Potential).  
 FT CARBOHYD 292 292 N-linked (GlcNAc. . . ) (Potential).  
 FT CARBOHYD 382 382 N-linked (GlcNAc. . . ) (Potential).  
 FT DISULFID 143 153 By similarity.  
 FT DISULFID 184 195 By similarity.  
 FT VARIANT 81 81 R -> H (in CISS).  
 FT VARIANT 374 374 /FTID=VAR\_017865.  
 FT VARIANT 240 240 L -> R (in CISS).  
 FT CONFLICT 240 240 D -> E (in Ref. 3).  
 SQ SEQUENCE 422 AA; 46302 MW; AD9DFCB01B84228 CRC64;  
 Query Match 93.1%; Score 2096; DB 1; Length 422;  
 Best Local Similarity 93.7%; Pred. No. 4.3e-158;  
 Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;  
 QY 1 MPAGRPGVAGSARPPRLPLSLMLLVGVRGGSGAHTAVISPODPTLLIGSSIQ 60  
 DB 1 MPAGRGPAGSARPP-PLPLLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57  
 QY 61 ATCSIHGTPGATAGLYWTNLNRRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 58 ATCSVHGPPGATAGLYWTNLNRRPLPELSRLNASTLALANLNGSRQSGDNLVCH 117  
 QY 121 ARDSGILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTPGAGHGTFLHTNYSKYKLRW 180  
 DB 118 ARDSGILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTPGAGHGTFLHTNYSKYKLRW 177  
 QY 181 YGQDNTCEYHTVGPCHSKIPKDLALFPEYIWEATNRLGARSDDLTLVDLVVTTDP 240  
 DB 178 YGQDNTCEYHTVGPCHSKIPKDLALFPEYIWEATNRLGARSDDLTLVDLVVTTDP 237  
 QY 241 PPDVHVSRVGGLDQLSVRWVSPALDKFLPAQKQIRYRVEDSVDMKVVDDVSNQTSR 300  
 DB 238 PPDVHVSRVGGLDQLSVRWVSPALDKFLPAQKQIRYRVEDSVDMKVVDDVSNQTSR 297  
 QY 301 LAGLPGTVTVVQVRCNPFPGIYGSKKAGIWSHPTAASPTSRSPRPGGVCPRGGE 360  
 DB 298 LAGLPGTVTVVQVRCNPFPGIYGSKKAGIWSHPTAASPTSRSPRPGGVCPRGGE 357  
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSPLRYDQWRNMOKSHKTNQ---VLPA 411  
 DB 358 PSSGPVRELKQFLGWLKKHAYCSNLSPLRYDQWRNMOKSHKTRNQEGLILPS 411  
 RESULT 3  
 Q6DG28 BRARE  
 ID Q6DG28 BRARE PRELIMINARY; PRT; 389 AA.  
 AC Q6DG28;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

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25-OCT-2004 (TREMBlrel. 28, Last annotation update)
Zgc:91992.
ORFNames=zgc:91992;
Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Strausberg R.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC EMBL: BC076526; AAH76526.1; -; mRNA.
DR ZFIN: ZDB-GENE-040718-397; Zgc:91992.
DR InterPro: IPR002996; Cytnk_recept_B/G.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS00853; FN3; 2.
DR Receptor; Repeat; Transmembrane.
KW SEQUENCE 389 AA; 43314 MW; E30903B99639064A CRC64;
SQ
Query Match 63.2%; Score 1422.5; DB 2; Length 389;
Best Local Similarity 68.2%; Pred. No. 1.4e-104;
Matches 262; Conservative 48; Mismatches 67; Indels 7; Gaps 5;
QY 27 LLLCVLGVPRGSGAHTAVISQDPTLLIGSSLOATCSIHGTPGATAGLYWTNGRRL 86
DB 7 LHLCAAGVL--SSSTQVATVYPQDPALLIGSSLTATCSVNPDP-HGIHAGSLYWTNGKRL 63
QY 87 PSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSLCYVGLPPEKPNISC 146
DB 64 PSSTYSILSPVTSVTLPRLSGSRQSGDNLVCHNGGHVLAGSLCYVGMPPKPNLTC 123
QY 147 WSNMMDLTCRWTPGAHGTFLHTNYSLKYLWYQGDNTCEBYHTVGPHSCHIPKDLAL 206
DB 124 WSNRTKDLTCRWAPGGGGETFIKTKYLYKLWYGREKECEDYSTGEPTCYIPDLAL 183
QY 207 FTPYEIWEATNRLGARSVDLFDLVDTVTTPDPDVHVSVRVGGLEDQLSVRWVSPPAL 266
DB 184 FTPYEIWEASNLGATSDVILDLVDVTTPDPDVHVSVRVGGLEDQLTVRWGTPPAL 243
QY 267 KDFLFQAKYQIRVRVEDSVMDKVDVDSNQTSCRLAGLKPGTVYFVQVRCNPRGIYGSKK 326
DB 244 KDFLFQAKYQIRVRLDEESSDKWKVDVDSNQTSCRLAGLRGTFTFVQVRCNPRVGLIGSRK 303
QY 327 AGIWSHSHPTAASTPRSERPGCGGVCYCPGSPGPRRELKQFLGWLKHKAY--CSN 385
DB 304 AGIWSHSHPTAASTPRSERLLTGS--CDSKAGQONS--TLRRDLKQFFGWVRKHAHGCSG 360
QY 386 LSFRLYDQWRAMQKSHKTRNQVL 409
DB 361 MSIKLYDQWRVWLQKSHKTRNQVL 384
RESULT 4
Q6UA05_TETNG PRELIMINARY; PRT; 394 AA.
AC Q6UA05;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Class I helical cytokine receptor number 1.
GN Name=CRPAI;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bilmont C., Skalli Z., Cattolico L., Poulain J., Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigs R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C.,
RA Wincker P., Schachter E.S., Weissenbach J., Crolius H.R.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957 (2004).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC EMBL: AY374473; AAR25664.1; -; mRNA.
DR Ensembl: AY374473; Tetraodon nigroviridis.
DR GO: GO:004872; F:receptor activity; IEA.
DR InterPro: IPR002996; Cytnk_recept_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS00853; FN3; 2.
DR Receptor; Repeat; Transmembrane.
KW Immunoglobulin domain; Receptor; Repeat; Transmembrane.
SQ SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;
Query Match 61.4%; Score 1382.5; DB 2; Length 394;
Best Local Similarity 67.7%; Pred. No. 2.2e-101;
Matches 260; Conservative 39; Mismatches 80; Indels 5; Gaps 4;
QY 27 LLLCVLGVPRG--GSGAHTAVISQDPTLLIGSSLOATCSIHGTPGATAGLYWTNGRR 85
DB 9 LLLLIHSPAVLALSTHVAIVYQDPFLRMGSLNLTASCLWRSDL-GVHASSLFWTLNGQP 67
QY 86 LPSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSLCYVGLPPEKPNIS 145
DB 68 LPSSLYRVLSPTNLVTLAGLNASRQTSGDNLVCHHHKHHILAGSLCYVGMPPKPNLT 127
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QY 146 CWSRNKDLTCRWTPGAGHETFLHTNYSYKYLRTWYGQDNTCEYHTVGPSPHSCHIPKDLA 205  
 DB 128 CWSRNKDLTCRWTPGAGHETFLHTNYSYKYLRTWYGQDNTCEYHTVGPSPHSCHIPKDLA 187  
 QY 206 LFTPEIWEATNRLGARSADVLTLVDVLTDPDPVHVSRVGGLEDQLSVRWVSPPA 265  
 DB 188 LFTPEIWEATNRLGARSADVLTLVDVLTDPDPVHVSRVGGLEDQLSVRWVSPPA 247  
 QY 266 LKDFLFOAKYQIRYRVEDSDVWVDDVSNQTSCLAGLPGTVYFVQVRCNPPFGYGSK 325  
 DB 248 LKDFLFOAKYQIRYRVEDSDVWVDDVSNQTSCLAGLPGTVYFVQVRCNPPFGYGSK 307  
 QY 326 KAGINSEWHPHTAASPRERPGCGVCEPRGSGPVRRELKQFLGWLKHHAY-CS 384  
 DB 308 KAGINSEWHPHTAASPRERPGCGVCEPRGSGPVRRELKQFLGWLKHHAY-CS 365  
 QY 385 NLSFRLYDQWRAMQKSHKTRNOV 408  
 DB 366 SMSMKLYDQWRVLMQKSHKARNOV 389

## RESULT 5

Q4RMP5\_TETNG  
 ID Q4RMP5\_TETNG PRELIMINARY; PRT; 437 AA.  
 AC Q4RMP5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE Chromosome 10 SCAR15019, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG00031935001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segrens B.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Bionet C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; CAAC01015019; CAG10337.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 437 AA; 49065 MW; 99F9602E88F95583 CRC64;

Query Match 44.2%; Score 995; DB 2; Length 437;  
 Best Local Similarity 53.8%; Pred. No. 1.6e-70;  
 Matches 199; Conservative 33; Mismatches 62; Indels 76; Gaps 5;  
 QY 44 AVTSPDPTLLTGSSLOATCSHGTPGATAGLWTLNGLRPLPSLSLNTSTLALAL 103  
 DB 1 AVTSPDPTLLTGSSLOATCSHGTPGATAGLWTLNGLRPLPSLSLNTSTLALAL 59

QY 104 ANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEKFPNISCWSNMKDLTCRWTPGAH 163  
 DB 60 AGLNASROTSGDNLVCHARDGSIAGSCLYVGLPPEKFPNISCWSNMKDLTCRWTPGAH 119  
 QY 164 GTEFLHTNYSYKYLRTWYGQDNTCEYHTVGPSPHSCHIPKDLAFTPEIWEATNRLGSA 223  
 DB 120 GTHISTQYTLKYLRTWYGQDNTCEYHTVGPSPHSCHIPKDLAFTPEIWEATNRLGSA 179  
 QY 224 RSDVLTLVDVLTDPDPVHVSRVGGLEDQLSVRWVSPPAKDFLFOAKYQIRYRVED 283  
 DB 180 TSDVITLVDVLTDPDPVHVSRVGGLEDQLSVRWVSPPAKDFLFOAKYQIRYRVED 239  
 QY 284 SDVWK-----VVDD 292  
 DB 240 SDVWK-----VVDD 299  
 QY 293 VSNQTSCLAGLPGTVYFVQVRCNPPFGYGSKAG-----IWSHSHPTAASPRERPG 348  
 DB 300 VGNQTSCLAGLPGTVYFVQVRCNPPFGYGSKAG-----IWSHSHPTAASPRERPG 339  
 QY 349 PGGVCEPRG 358  
 DB 340 ASAGPLQPRG 349

## RESULT 6

Q4TCM7\_TETNG  
 ID Q4TCM7\_TETNG PRELIMINARY; PRT; 207 AA.  
 AC Q4TCM7\_TETNG  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAP6801, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG0003230001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segrens B.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Bionet C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; CAAC01006801; CAF89355.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 207 AA; 22607 MW; 71F8E80B9998309F CRC64;

Query Match 20.8%; Score 468.5; DB 2; Length 207;  
 Best Local Similarity 48.3%; Pred. No. 4.6e-29;  
 Matches 102; Conservative 7; Mismatches 21; Indels 81; Gaps 4;

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QY 231 DVLVDVTTDPPDPVHVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVWK-- 288
Db 1 ECLPVTTPDPPSGVTVSRVQLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVWKEE 60
QY 289 -----VDDVSNQTS 299
Db 61 KSAFQERERAWTEPLCILGLRLVLMNEKYSVEAGPLQWALLRILLPVLVMDVGNQTS 120
QY 300 RLALGLKPGTVY-----FVQVRCNPFYIGSKKAGIWSHPT 337
Db 121 RLALGLRPGTVYSRWDPGPAPQTGSGSLTAVSLPQVRCNPFYIGSKKAGIWSHPT 180
QY 338 AASTPRSERP-----GPGGVGVCBPRGEPSSG 364
Db 181 AASTPHSGEPPLPAGPGRSL-----GSAPRSG 207

RESULT 7
Q4RD1 TETNG PRELIMINARY; PRT; 151 AA.
AC Q4RD1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15947, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037335001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015947; CAG13471.1; -; Genomic_DNA.
FT NON_TER 151
SQ SEQUENCE 151 AA; 16177 MW; 14AD74333A6C7F90 CRC64;

Query Match 18.5%; Score 416; DB 2; Length 151;
Best Local Similarity 58.0%; Pred. No. 4.6e-25;
Matches 80; Conservative 15; Mismatches 37; Indels 6; Gaps 2;

QY 29 LCVLGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPTCATAGLWTWTLNGLRPLS 88
Db 20 VCVV-----GHPDVAEVSQDPVLPITGSSLTATCTLSPEL-RLLSALYWTWTLNGLTLP 73
QY 89 ELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSLYGLPPEKPFNTSCWS 148
Db 74 STYGRIGPHTLSVTLHNLNGSRQSGDNLVCHSDGHLVAGACLYGMPPEKPNLTCWS 133
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QY 149 RNKDLTCRWTPCAHGET 166
Db 134 RNTKDLSCRWPRPGLGET 151

RESULT 8
Q4RD9 TETNG PRELIMINARY; PRT; 199 AA.
AC Q4RD9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15948, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037750001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015948; CAG13473.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 199 AA; 21734 MW; 299786CDFB24BDEB CRC64;

Query Match 16.9%; Score 380; DB 2; Length 199;
Best Local Similarity 67.0%; Pred. No. 4.7e-22;
Matches 73; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 236 VTTDPPDPVHVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVWKVDDVSN 295
Db 34 VTTDPTDVHVSQVGGDLDDQLTVRTWSPDLEILFQAKYQIRYRVEDSNEWKV----- 87
QY 296 QTSCLAGLKPQTVYFVQVRCNPFYIGSKKAGIWSHPTAAPTSP 344
Db 88 -----SVLWTVHFVQVRCNPFYIGSKKAGIWSHPTAAPTSP 128

RESULT 9
Q9W6U9 CHICK PRELIMINARY; PRT; 918 AA.
AC Q9W6U9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glycoprotein 130 precursor.
GN Name=Gp130;
OS Gallus gallus (Chicken).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryonic heart primary culture;  
 RX MEDLINE=99026068; PubMed=9806927;  
 RA Geissen M., Heller S., Pennica D., Ernberger U., Rohrer H.;  
 RT "The specification of sympathetic neurotransmitter phenotype depends  
 on gp130 cytokine receptor signaling.";  
 RL Development 125:4791-4801(1998).  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 folding and thereby efficient intracellular transport and cell-  
 surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 activation (By similarity).  
 CC activation (By similarity).  
 DR EMBL: AJ011688; CAB42084.1; -; mRNA.  
 DR HSP; P40189; IBQ9.  
 DR InterPro: IPR002996; Cytn\_recept\_B/G.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR003529; Hemtrecept\_1302.  
 DR InterPro: IPR010457; Lep\_receptor\_Ig.  
 DR Pfam: PF00041; fn3; 4.  
 DR Pfam: PF06328; Lep\_receptor\_Ig; 1.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS00853; FN3; 5.  
 DR PROSITE; PS01353; HENATOPO\_REC\_L\_F2; UNKNOWN\_1.  
 KW Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 26 Potential.  
 SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613EF CRC64;  
 Query Match 16.5%; Score 371; DB 2; Length 918;  
 Best Local Similarity 30.2%; Pred. No. 1.7e-20;  
 Matches 111; Conservative 41; Mismatches 138; Indels 78; Gaps 16;  
 QY 27 LLLCVLGVPRGSGAHTAVISQDPTLLIGSSLIQATCSIHG---DTPGATAGLYWTLMG 83  
 Db 16 LNICSEV-SGGVQSCGHIIPESPVLALGNSFTALCILNESCLDPGNIYASQIIWMKN 74  
 QY 84 RLPLSELSLLN-----TSTLALALANLNGSRQSGDNLVCHA-RDGSI---LAG 129  
 Db 75 KVIPKEQYREINRTVSSVTFNDTSSLA-----SPLTCNLVADGQIEQNIYG 120  
 QY 130 SCLVGLPEKPFNISC-----WSRNMKDLTCRWTPGAGHGTFLHTNYSKYKLW 180  
 Db 121 ISVTGLPEKPNLSIVLSPKVEWYN-----CTWNPGRH--TFDTRFLKTMWPR 173  
 QY 181 YGQDNTCEYHTVGPSCCHIPKD LALFTPYEIVWEATNRLGARS DVLTLVDVVVTTDP 240  
 Db 174 ETFFDCIPEYVN---NSCTI-SDVQFFVNLEWVEAALGKAESDHLVFDPIEVKPPP 229  
 QY 241 PPDVHVS RVGGLEDQLSVRWSPPAL KDPLFOAKYQIRVSDVDWKV---DVSNOT 297  
 Db 230 PRLSVNS-GILPTVLKLSWEN-QISTVVMELKNIRYRISGDTNMEVPPEDTASPT 286  
 QY 298 SCLAGLKPGTVYFVQVRCNPGIYSGKAGIWESEHPTASTPRSRPFGGGVCEPR 357  
 Db 287 SFSIQGLRPYTYFVSIRC-----MKEDGVGFWSWDSEIQIGVTTED----- 328  
 QY 358 GGPSPSGP 365  
 Db 329 --KPSKGP 334  
 RESULT 10  
 O57519 XENLA  
 ID O57519 XENLA PRELIMINARY; PRT; 881 AA.  
 AC O57519;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Gp130p1.

GN Name=xgpl30;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Chen J., Grace A., Chien K.R.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 folding and thereby efficient intracellular transport and cell-  
 surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 activation (By similarity).  
 CC activation (By similarity).  
 DR EMBL: AF041845; AAC03531.1; -; mRNA.  
 DR HSP; P40189; IBJ8.  
 DR InterPro: IPR002996; Cytn\_recept\_B/G.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR003529; Hemtrecept\_1302.  
 DR InterPro: IPR010457; Lep\_receptor\_Ig.  
 DR Pfam: PF00041; fn3; 4.  
 DR Pfam: PF06328; Lep\_receptor\_Ig; 1.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS00853; FN3; 5.  
 DR PROSITE; PS01353; HENATOPO\_REC\_L\_F2; UNKNOWN\_1.  
 KW Receptor; Repeat; Transmembrane.  
 SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;  
 Query Match 15.8%; Score 355.5; DB 2; Length 881;  
 Best Local Similarity 30.5%; Pred. No. 2.8e-19;  
 Matches 100; Conservative 43; Mismatches 136; Indels 49; Gaps 11;  
 QY 50 DPTLLIGS-SLOATCSIHGDTPGATAGLYWTLMGERLPSELRLNTSTLALANLNG 108  
 Db 33 DPGIVHGERPFTAYCVINQTCLEBDAIRYWLKGVKPEVETQYEILNQTTSVTFENLT 92  
 QY 109 SRQSGDNLVCHARGDSILAGSLVGLPPEKPFNISCWSRNMKDLTCRWTPGAGHGTFL 168  
 Db 93 LNSPLTCNVMSAGHVNTLYGIFFTLGLPDPDFTNLTCIYVQDNLCTCTWDGPR--PTNL 150  
 QY 169 HTNYSKYKLW-----YGQDNTCEYHTVGPSCCHIPKD LALFTPYEIVWEATNRL 220  
 Db 151 PTNYTLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFQVEATNEL 198  
 QY 221 GSARSDVLTLDVLDVVTTDPPDPDVHVS RVGGLEDQLSVRWSPPAL KDPLFOAKYQIRY 280  
 Db 199 GIKQSETLTIDPVNTVKPNPQLSELISSELPNALKIEWKNPIT---NAFNLKYNIRY 255  
 QY 281 VEDSDVKV---DVSNOTSCRLAGLKPGTVYFVQVRCNPGIYSGKAGIWESEHPT 337  
 Db 256 PVKQDWEVPEEDTASHRDSFTLQDLLPNTVYVSIRC-----THKDHGFWSWDSELK 310  
 QY 338 AASTPRSRPFGGGVCEPRGSPSGP 365  
 Db 311 KQVTP-EAP-----PSRGP 323  
 RESULT 11  
 Q8TD78 HUMAN  
 ID Q8TD78 HUMAN PRELIMINARY; PRT; 268 AA.  
 AC Q8TD78;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Prolactin receptor delta 7/11.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=breast tumor;  
 RA Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation (By similarity).  
 CC EMBL; AF492470; AAM18048.1; -; mRNA.  
 DR HSSP; P16471; 1BP3.  
 DR SMR; Q87D78; 29-227.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003528; HemptreceptL\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS0853; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor.  
 SQ SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;  
 Query Match 14.7%; Score 332; DB 2; Length 268;  
 Best Local Similarity 37.0%; Pred. No. 4.5e-18;  
 Matches 84; Conservative 28; Mismatches 97; Indels 18; Gaps 8;  
 QY 126 ILAGSCLYVG-LPPEKPFNISCWSNMKDLTCRWTPGAHGETFLHNTYSLKYKLRWYQGD 184  
 Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTVHREGETLM 72  
 QY 185 NTCEEVHTVGRPSCHIPKD-LALFTPYEIVWEATNRLGARSDDLTLVDLVVTTDPPPD 243  
 Db 73 HCEPDYITGGPSCHFGKQYTSNWRYYIMVNATNQMGSSFSDLYVDVTVYVQDPDPLE 132  
 QY 244 VHSVRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVWKVDDVSNQTS 298  
 Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGWTFLYLRKPEKAAWE-IHFACQOTE 190  
 QY 299 CRLAGLKPGTVTVQVRCNPFGLYGSKKAGIWSWSHPTAASTPSE 345  
 Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAWSPATFIQIPSGD 230

RESULT 12  
 Q96P36 HUMAN  
 ID Q96P36\_HUMAN PRELIMINARY; PRT; 288 AA.  
 AC Q96P36;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Prolactin receptor short isoform 1b.  
 GN Name=PRLR;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=placenta;  
 RA Trott J.F., Hovey R.C., Vonderhaar B.K.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Hu Z.Z., Meng J., Dufau M.L.;  
 RA PubMed=11518703;  
 RT "Isolation and characterization of two novel forms of the human  
 RT prolactin receptor generated by alternative splicing of a newly  
 RT identified exon 11."

RL J. Biol. Chem. 276:41086-41094 (2001).  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation (By similarity).  
 DR EMBL; AF416618; AAL23914.1; -; mRNA.  
 DR PIR; B59405; B59405.  
 DR HSSP; P16471; 1BP3.  
 DR SMR; Q96P36; 29-227.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003528; HemptreceptL\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS0853; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor.  
 SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;  
 Query Match 14.7%; Score 331; DB 2; Length 288;  
 Best Local Similarity 37.5%; Pred. No. 6e-18;  
 Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;  
 QY 126 ILAGSCLYVG-LPPEKPFNISCWSNMKDLTCRWTPGAHGETFLHNTYSLKYKLRWYQGD 184  
 Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTVHREGETLM 72  
 QY 185 NTCEEVHTVGRPSCHIPKD-LALFTPYEIVWEATNRLGARSDDLTLVDLVVTTDPPPD 243  
 Db 73 HCEPDYITGGPSCHFGKQYTSNWRYYIMVNATNQMGSSFSDLYVDVTVYVQDPDPLE 132  
 QY 244 VHSVRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVWKVDDVSNQTS 298  
 Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGWTFLYLRKPEKAAWE-IHFACQOTE 190  
 QY 299 CRLAGLKPGTVTVQVRCNPFGLYGSKKAGIWSWSHPTAASTP 342  
 Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAWSPATFIQIP 227  
 RESULT 13  
 Q9UHJ5 HUMAN  
 ID Q9UHJ5\_HUMAN PRELIMINARY; PRT; 349 AA.  
 AC Q9UHJ5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Intermediate prolactin receptor isoform.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461;  
 RX Kline J.B., Roehrs H., Clevenger C.V.;  
 RA "Functional characterization of the intermediate isoform of the human  
 RT prolactin receptor."  
 RL J. Biol. Chem. 274:35461-35468 (1999).  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation (By similarity).  
 DR EMBL; AF166329; AAD49855.1; -; mRNA.  
 DR HSSP; P16471; 1BP3.  
 DR SMR; Q9UHJ5; 29-227.  
 DR GO; GO:0009986; C:cell surface; IDA.



RT "The human prolactin receptor gene structure and alternative promoter  
RT utilization: the generic promoter hP111 and a novel human promoter  
RT hP(N)".  
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).  
RC TISSUE=Mammary carcinoma;  
RA Kline J.B., Cleveland C.V.;  
RT "Characterization of a novel and functional human prolactin receptor  
RT isoform (delta-S1 PRLr) containing only one extracellular fibronectin-  
RT like domain".  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC TISSUE=Placenta;  
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
RT MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RT Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RT Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RT Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RT Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RT Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RT Fahy J., Helton E., Kettman A.C., Shevchenko Y., Bouffard G.G.,  
RA Whitling M., Madan A., Young A.C., Green E.D., Dickinson M.C.,  
RT Blakesley R.W., Touchwood J.W., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Skrzewski M.I., Skalska U., Smalhus D.E.,  
RT Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).  
RC TISSUE=Mammary carcinoma;  
RA MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;  
RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;  
RA Fuh G., Wells J.A.;  
RT "prolactin receptor antagonists that inhibit the growth of breast  
RT cancer cell lines".  
RL J. Biol. Chem. 270:13133-13137(1995).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.  
RX MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;  
RA Somers W., Ullrich M., de Vos A.M., Kossiakoff A.A.;  
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";  
RN Nature 372:478-481(1994).  
CC -|- FUNCTION: This is a receptor for the anterior pituitary hormone  
CC prolactin.  
CC -|- INTERACTION:  
CC P51956:NEK3; NbExp=1; IntAct=EBI-476182, EBI-476041;  
CC P52735:VAV2; NbExp=1; IntAct=EBI-476182, EBI-297549;  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1;  
CC IsoId=P16471-1; Sequence=Displayed;  
CC Name=2; Synonyms=Delta-S1;  
CC IsoId=P16471-2; Sequence=VSP\_001720;  
CC Name=3;  
CC IsoId=P16471-3; Sequence=VSP\_012620, VSP\_012621;  
CC Note=Soluble isoform that appears specific for the BT-474 breast  
CC cancer cell line;  
CC -|- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
CC folding and thereby efficient intracellular transport and cell-  
CC surface receptor binding.  
CC -|- DOMAIN: The box 1 motif is required for JAK interaction and/or  
CC activation.  
CC -|- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1  
CC subfamily.

CC CC -|- SIMILARITY: Contains 2 fibronectin type-III domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M31661; AAA60174.1; -; mRNA.  
DR EMBL; AF091870; AAD32032.1; -; Genomic DNA.  
DR EMBL; AF091863; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF091864; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF091865; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF091866; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF091867; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF091868; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF091869; AAD32032.1; JOINED; Genomic DNA.  
DR EMBL; AF349939; AAK32703.1; -; mRNA.  
DR EMBL; BC059392; AAHS9392.1; -; mRNA.  
DR EMBL; S78505; AAB34470.1; -; mRNA.  
DR PIR; A40144; A40144.  
DR PDB; 1BP3; X-ray; B=25-235.  
DR IntAct; P16471; -;  
DR Ensembl; ENSG00000113494; Homo sapiens.  
DR HGNC; HGNC:9446; PRLR.  
DR MIM; 176761; -;  
DR GO; GO:0009986; C:cell surface; IDA.  
DR GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.  
DR GO; GO:0004925; F:prolactin receptor activity; NAS.  
DR GO; GO:0042803; F:protein homodimerization activity; NAS.  
DR GO; GO:0006936; P:anti-apoptosis; NAS.  
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.  
DR GO; GO:0007595; P:embryo implantation; TAS.  
DR GO; GO:0006694; P:steroid biosynthesis; NAS.  
DR GO; GO:0042110; P:T cell activation; NAS.  
DR GO; GO:00042977; P:tyrosine phosphorylation of JAK2 protein; NAS.  
DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR003528; HemptreceptL\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR PROSITE; PS50853; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW 3D-structure; Alternative splicing; Glycoprotein; Receptor; Repeat;  
KW Signal; Transmembrane.  
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FT CHAIN 25 622  
FT TOPO\_DOM 25 234  
FT TRANSMEM 235 258  
FT TOPO\_DOM 259 622  
FT DOMAIN 27 121  
FT DOMAIN 127 227  
FT MOTIF 215 219  
FT MOTIF 267 275  
FT CARBOHYD 59 59  
FT CARBOHYD 104 104  
FT CARBOHYD 233 233  
FT DISULFID 36 46  
FT DISULFID 75 86  
FT VARSPPLIC 24 124  
FT VARSPPLIC 229 230  
FT VARSPPLIC 231 622  
FT STRAND 31 38  
FT STRAND 44 50  
FT STRAND 61 66  
FT STRAND 73 74  
FT TURN 80 81  
FT STRAND 85 88  
FT TURN 91 92



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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:16:39 ; Search time 28.5393 Seconds  
(without alignments)  
1196.422 Million cell updates/sec

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Perfect score: 2251  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCUTS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2197.5	97.6	425	2	US-09-071-224-6
2	2119	94.1	407	2	US-09-521-335-13
3	2118.5	94.1	405	2	US-09-012-072-2
4	2118.5	94.1	405	2	US-09-120-601-2
5	2114.5	93.9	410	2	US-09-521-335-12
6	2098	93.2	425	2	US-09-071-224-4
7	2096	93.1	422	2	US-09-866-028-32
8	2096	93.1	422	2	US-09-944-457-32
9	2096	93.1	422	2	US-09-945-584-32
10	2096	93.1	422	2	US-09-944-944-32
11	2096	93.1	422	2	US-09-945-587-32
12	2092	92.9	422	2	US-09-071-224-2
13	2075.5	92.2	448	2	US-09-120-601-6
14	2015.5	89.5	434	2	US-09-012-072-4
15	2015.5	89.5	434	2	US-09-120-601-4
16	2006.5	88.1	385	2	US-09-071-224-19
17	1982	88.0	392	2	US-09-071-224-18
18	1970.5	87.5	388	2	US-09-071-224-17
19	1967	87.4	389	2	US-09-071-224-28
20	1966	87.3	389	2	US-09-071-224-22
21	1965	87.3	389	2	US-09-071-224-29
22	1964	87.3	389	2	US-09-071-224-30
23	1963	87.2	389	2	US-09-071-224-24
24	1963	87.2	389	2	US-09-071-224-25
25	1963	87.2	389	2	US-09-071-224-27
26	1962	87.2	389	2	US-09-071-224-26
27	1961	87.1	389	2	US-09-071-224-31

28 1954.5 86.8 385 2 US-09-071-224-20 Sequence 20, Appl  
29 1602 71.2 303 2 US-09-071-224-23 Sequence 23, Appl  
30 1598 71.0 303 2 US-09-071-224-21 Sequence 21, Appl  
31 334 14.8 1168 2 US-09-313-942-24 Sequence 24, Appl  
32 334 14.8 1168 2 US-10-282-162-24 Sequence 24, Appl  
33 331 14.7 332 2 US-09-313-942-10 Sequence 10, Appl  
34 331 14.7 332 2 US-10-282-162-10 Sequence 10, Appl  
35 331 14.7 349 2 US-08-806-597A-14 Sequence 14, Appl  
36 331 14.7 349 2 US-08-970-016-10128 Sequence 14, Appl  
37 331 14.7 637 2 US-09-949-016-10128 Sequence 10128, A  
38 331 14.7 1158 2 US-09-313-942-26 Sequence 26, Appl  
39 331 14.7 1158 2 US-10-282-162-26 Sequence 26, Appl  
40 329 14.6 488 1 US-08-599-455B-5 Sequence 5, Appl  
41 329 14.6 488 2 US-09-069-781B-5 Sequence 5, Appl  
42 329 14.6 488 2 US-09-137-132-5 Sequence 5, Appl  
43 329 14.6 488 2 US-08-864-564A-5 Sequence 5, Appl  
44 329 14.6 488 2 US-09-094-410-5 Sequence 5, Appl  
45 329 14.6 488 2 US-08-708-123D-5 Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-071-224-6  
; Sequence 6, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-071-224-6

Query Match 97.6%; Score 2197.5; DB 2; Length 425;  
Best Local Similarity 97.6%; Pred. No. 4.4e-197;  
Matches 404; Conservative 3; Mismatches 4; Indels 3; Gaps 1;  
  
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DB 1 MPAGGPGPAAQARRPRRLSSLSWPLLLCVLGVPPQGGGAHTAVISPODPTLLIGSSILH 60  
  
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DB 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180  
  
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DB 301 LAGLKPGTVYVQVRCNPFGIYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGE 360  
  
QY 361 PSSGPPVRRRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
DB 361 PSSGPPVRRRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 2  
US-09-521-335-13  
; Sequence 13, Application US/09521335  
; Patent No. 6800460  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/09/521,335  
; CURRENT FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: rodent  
US-09-521-335-13

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DB 1 RPLSSLSWPLLLCVLGVPRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 60  
  
QY 78 YWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137  
DB 61 YWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119  
  
QY 138 PEKFPNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGDNTCEEYHTVGPSS 197  
DB 120 PEKFPNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGDNTCEEYHTVGPSS 179  
  
QY 198 CHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLDVVTDPDPDVHVSRYVGGLEDQLS 257

DB 180 CHIPKDLALFTPEIWEATNRLGSARSDVLTLDVLDVVTDPDPDVHVSRYVGGLEDQLS 239  
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DB 300 PFGIYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPPVRRRELKQFLGWL 359  
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DB 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 396

RESULT 3  
US-09-012-072-2  
; Sequence 2, Application US/09012072  
; Patent No. 6060276  
; GENERAL INFORMATION:  
; APPLICANT: Masiakowski, Piotr  
; TITLE OF INVENTION: No. 6060276el Orphan Receptors  
; FILE REFERENCE: REG 630  
; CURRENT APPLICATION NUMBER: US/09/012,072  
; CURRENT FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: MOUSE  
US-09-012-072-2

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Best Local Similarity 98.7%; Pred. No. 1e-189;  
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QY 81 LNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 140  
DB 61 LNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 120  
  
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DB 121 PFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGDNTCEEYHTVGPSSCHI 180  
  
QY 201 PKDLALFTPEIWEATNRLGSARSDVLTLDVLDVVTDPDPDVHVSRYVGGLEDQLSVRW 260  
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QY 261 VSPALKDFLFOAKYQIRYRVDSVDKVVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPF 320  
DB 241 VSPALKDFLFOAKYQIRYRVDSVDKVVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPF 300  
  
QY 321 IYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPPVRRRELKQFLGMLKCH 380  
DB 301 IYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPPVRRRELKQFLGMLKCH 360  
  
QY 381 AYCNSLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
DB 361 AYCNSLSFRLYDQWRAMQKSHKTRNQDEGILPS 394

RESULT 4  
US-09-120-601-2  
; Sequence 2, Application US/09120601  
; Patent No. 6207413  
; GENERAL INFORMATION:  
; APPLICANT: Masiakowski, Piotr  
; TITLE OF INVENTION: No. 6207413el Orphan Receptors

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; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
; US-09-120-601-2

Query Match          94.1%; Score 2114.5; DB 2; Length 405;
Best Local Similarity 98.7%; Pred. No. 1e-189;
Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

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DB 121 PFNISCWSRNKDLTCRWTPPGAHTFHLTNTSLKYKRWYQDNTCEEYHTVGPHSCHI 180
QY 201 PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSVRVGGLEDQLSVRW 260
DB 181 PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSVRVGGLEDQLSVRW 240
QY 261 VSPPALKDFLOAKQIRYRVSDSVDMKVVDVSNQTSCLRLAGLKPVTYFVQVRCNPG 320
DB 241 VSPPALKDFLOAKQIRYRVSDSVDMKVVDVSNQTSCLRLAGLKPVTYFVQVRCNPG 300
QY 321 IYGGKAGIWSWSHPTAASTPRSRPFGGVCBPRGSGVPRRELKQFLGWLKXH 380
DB 301 IYGGKAGIWSWSHPTAASTPRSRPFGGVCBPRGSGVPRRELKQFLGWLKXH 360
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DB 361 AYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 394

RESULT 5
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; Sequence 12, Application US/09521335
; Patent No. 6800460
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazzan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
; US-09-521-335-12

Query Match          93.9%; Score 2114.5; DB 2; Length 410;
Best Local Similarity 94.7%; Pred. No. 2.5e-189;
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

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DB 1 MPAGRRGPVAGSARRPPRLPSLSWSPLLLCVIGVPRGSGAHTAVISPODPTLLIGSSLLQ 57
QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELSRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSIHGDTPGATAGLYWTLNGRLPSELSRLNTSTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWSRNKDLTCRWTPPGAHTFHLTNTSLKYKRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWSRNKDLTCRWTPPGAHTFHLTNTSLKYKRW 177
QY 181 YQDNTCEEYHTVGPHSCHI PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPP 240
DB 178 YQDNTCEEYHTVGPHSCHI PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPP 237
QY 241 PDVHVSVRVGGLEDQLSVRWSPPALKDFLOAKQIRYRVSDSVDMKVVDVSNQTSCL 300
DB 238 PDVHVSVRVGGLEDQLSVRWSPPALKDFLOAKQIRYRVSDSVDMKVVDVSNQTSCL 297
QY 301 LAGLKPVTYFVQVRCNPGIYGGKAGIWSWSHPTAASTPRSRPFGGVCBPRGSG 360
DB 298 LAGLKPVTYFVQVRCNPGIYGGKAGIWSWSHPTAASTPRSRPFGGVCBPRGSG 357
QY 361 PSSGVRRELKQFLGWLKXHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPAKL 413
DB 358 PSSGVRRELKQFLGWLKXHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPAKL 410

RESULT 6
US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: ZymoGenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-4

Query Match      93.2%; Score 2098; DB 2; Length 425;
Best Local Similarity 91.1%; Pred. No. 9,1e-188;
Matches 391; Conservative 5; Mismatches 13; Indels 20; Gaps 3;

QY 1 MPAGRPGVPAQASARRPPPLSLWSPLLLCVLGVPRGSGAHTAVISQDPTLLIGSSILQ 60
DB 1 MPAGRRGPAQASARRPP-PLPLPL---LLLCVLGAPRAGSGAHTAVISQDPTLLIGSSULL 56
QY 61 ATCSITHGDTPGATAGLWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 57 ATCSVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCH 116
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 117 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176
QY 181 YQDNTCEHYTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVDVVTDP 240
DB 177 YQDNTCEHYTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVDVVTDP 236
QY 241 PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR 300
DB 237 PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR 296
QY 301 LAGLKPVTYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSRPGRGGVCPBPGGE 360
DB 297 LAGLKPVTYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSRPGRGGVCPBPGGE 356
QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ-----407
DB 357 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ-----407

QY 408 ---VLPAKL 413
DB 417 RREVLPDKL 425

RESULT 7
US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; TYPE: PRT
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; ORGANISM: Homo Sapien
US-09-866-028-32

Query Match      93.1%; Score 2096; DB 2; Length 422;
Best Local Similarity 93.7%; Pred. No. 1.4e-187;
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGVPAQASARRPPPLSLWSPLLLCVLGVPRGSGAHTAVISQDPTLLIGSSILQ 60
DB 1 MPAGRRGPAQASARRPP-PLPLPL---LLLCVLGAPRAGSGAHTAVISQDPTLLIGSSULL 57
QY 61 ATCSITHGDTPGATAGLWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177
QY 181 YQDNTCEHYTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVDVVTDP 240
DB 178 YQDNTCEHYTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVDVVTDP 237
QY 241 PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR 300
DB 238 PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR 297
QY 301 LAGLKPVTYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSRPGRGGVCPBPGGE 360
DB 298 LAGLKPVTYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSRPGRGGVCPBPGGE 357
QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
DB 358 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 411

RESULT 8
US-09-944-457-32
; Sequence 32, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; TYPE: PRT
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;; PRIOR FILING DATE: December 12, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,696  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,694  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,702  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,870  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,873  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/068,017  
;; PRIOR FILING DATE: December 18, 1997  
;; PRIOR APPLICATION NUMBER: 60/070,440  
;; PRIOR FILING DATE: January 5, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,086  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,092  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/075,945  
;; PRIOR FILING DATE: February 25, 1998  
;; PRIOR APPLICATION NUMBER: 60/112,850  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 60/113,296  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 60/146,222  
;; PRIOR FILING DATE: July 28, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: September 16, 1998  
;; PRIOR APPLICATION NUMBER: PCT/US98/25108  
;; PRIOR FILING DATE: December 1, 1998  
;; PRIOR APPLICATION NUMBER: 09/216,021  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 09/218,517  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 09/254,311  
;; PRIOR FILING DATE: March 3, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: June 22, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: September 15, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28409  
;; PRIOR FILING DATE: No. 673428member 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: No. 673428member 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28301  
;; PRIOR FILING DATE: December 1, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: December 16, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: February 11, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: February 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: March 2, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/08439  
;; PRIOR FILING DATE: March 30, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: May 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/20710  
;; PRIOR FILING DATE: July 28, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: February 28, 2001  
;; NUMBER OF SEQ ID NOS: 120  
;; SEQ ID NO 32  
;; LENGTH: 422  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien

US-09-944-457-32

Query Match 93.1%; Score 2096; DB 2; Length 422;

Best Local Similarity 93.7%; Pred. No. 1.4e-187;  
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;  
QY 1 MPAGRRGVAQSAARRPPRLSSLSWFLLCVTVGRGGSGAHTAVTSPDPTLLIGSSLLQ 60  
Db 1 MPAGRRGVAQSAARRPP-PLLP-LL-LLCVCVLAGPAGSGAHTAVTSPDPTLLIGSSLL 57  
QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELSSLLANTSTLALANLNGSRQSGDNLVCH 120  
Db 58 ATCSVHGDPGATAGLYWTLNGRLPSELSSVLANASTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAGHTFLLHTNYSLYKLRW 180  
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAGHTFLLHTNYSLYKLRW 177  
QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEITWVETATNPLGSARSDVLTLDVLDVVTDP 240  
Db 178 YQDNTCEYHTVGPHSCHIPKDLALFTPYEITWVETATNPLGSARSDVLTLDVLDVVTDP 237  
QY 241 PPDVHVSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVDSNQTSCR 300  
Db 238 PPDVHVSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVDSNQTSCR 297  
QY 301 LAGLKPCTVYFVQVRCNPFYIGSKAGIWSWSHPTAASRPRSRPGRGGVCEPRGGE 360  
Db 298 LAGLKPCTVYFVQVRCNPFYIGSKAGIWSWSHPTAASRPRSRPGRGGVCEPRGGE 357  
QY 361 PSSGPVRELBKQFLGWLKXKHCAYCSNLSPLDYDQWRAWQKSHKTRNQ---VLP 411  
Db 358 PSSGPVRELBKQFLGWLKXKHCAYCSNLSPLDYDQWRAWQKSHKTRNQDEGILPS 411

RESULT 9

US-09-945-584-32  
; Sequence 32, Application US/09945584  
; Patent No. 6908993  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,584  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694



PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/069,873  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/068,017  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,092  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 60/113,296  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 60/146,222  
 PRIOR FILING DATE: July 28, 1999  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/254,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28409  
 PRIOR FILING DATE: No. 6929947ember 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: No. 6929947ember 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28301  
 PRIOR FILING DATE: December 1, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: December 16, 1999  
 PRIOR APPLICATION NUMBER: PCT/US00/03565  
 PRIOR FILING DATE: February 11, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: February 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: March 2, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/08439  
 PRIOR FILING DATE: March 30, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/14042  
 PRIOR FILING DATE: May 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/20710  
 PRIOR FILING DATE: July 28, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: December 1, 2000  
 PRIOR APPLICATION NUMBER: PCT/US01/06520  
 PRIOR FILING DATE: February 28, 2001  
 NUMBER OF SEQ ID NOS: 120  
 SEQ ID NO 32  
 LENGTH: 422  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-944-944-32

Query Match 93.1%; Score 2096; DB 2; Length 422;  
 Best Local Similarity 93.7%; Pred. No. 1.4e-187;  
 Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPQPAQAARRPRPLSLWSPLLICVLGVPKGGSGAHTAVISPDPTLLIGSLQ 60  
 DB 1 MPAGRGPAQAARRPP-FLLELL--LLLCVUGAPRAGSGAHTAVISPDPTLLIGSL 57  
 Y 61 ATCSIHGDTPGTAEGLYWTLNGRLPSELSRLMTSTLTALANLINGSRQSGDNLVCH 120

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; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-32

Query Match          93.1%; Score 2096; DB 2; Length 422;
Best Local Similarity 93.7%; Pred. No. 1.4e-187;
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

Qy      1  MPAGRGPGVQAQARRPPRLSSLLWSPLLLCVLGPRGSGAHTAVISPQDPTLLIGSSLQ 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1  MPAGRRGPAQAARRPP-PLLP-L-LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSL 57
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy      61  ATCSIHGDTFGAETAGLYWTNGRRRLPSELRLNTSTLALANLNGSQSGSDNLVCH 120
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Db      58  ATCSVHGDPGATAGLYWTNGRRRLPPELSELRLNASTLALANLNGSRQSGSDNLVCH 117
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy      121  ARDGSILAGSLYVGLPPEKPFNISCWNRNMKDLTCRWTFGAHGETFLHTNYSIKYKLRW 180
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Db      118  ARDGSILAGSLYVGLPPEKPFNISCWNRNMKDLTCRWTFGAHGETFLHTNYSIKYKLRW 177
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy      181  YQODNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLFLDVLDDVTTDP 240
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      178  YQODNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLFLDVLDDVTTDP 237
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy      241  PPDVHVSRYGGLLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      238  PPDVHVSRYGGLLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 297
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy      301  LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPFGGGVCEPRGGE 360
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      298  LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPFGGGVCEPRGGE 357
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy      361  PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSKHKTRNQ---VLPA 411
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      358  PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSKHKTRNQDEGILPS 411
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 12
US-09-071-224-2
; Sequence 2, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-2

Query Match          92.9%; Score 2092; DB 2; Length 422;
Best Local Similarity 93.5%; Pred. No. 3.3e-187;
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Matches 387; Conservative 8; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGPVAQARRPPRLSSLSWSPLLLCVLGPRGSGAHTAVISPDPTLLIGSSILQ 60

Db 1 MPAGRRGPAAQARRPP-PLLPL--LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLL 57

QY 61 ATCSIHGDPGATAEGLYTLNGRRLLPSBLRLLNTSTLALANLNGSRQSGDNLVCH 120

Db 58 ATCSVHGDPGATAEGLYTLNGRRLLPSBLRLLNTSTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKVKLRW 180

Db 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKVKLRW 177

QY 181 YQDNTCEBYHTVGPCHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDLVVTTDP 240

Db 178 YQDNTCEBYHTVGPCHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDLVVTTDP 237

QY 241 PDVHVSRVGGLEDQLSVRWSPALKDFLFOAKYQIRYRVSDVWKVDDVSNQTSR 300

Db 238 PPEVHVSRRVGGLEDQLSVRWSPALKDFLFOAKYQIRYRVSDVWKVDDVSNQTSR 297

QY 301 LAGLKPCTVYFVQVRCNPFYVGSKKAGIWSKSHPTAASTPRSERPGGVCBPRGGE 360

Db 298 LAGLKPCTVYFVQVRCNPFYVGSKKAGIWSKSHPTAASTPRSERPGGVCBPRGGE 357

QY 361 PSSGPRVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411

Db 358 PSSGPRVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 411

RESULT 13

US-09-120-601-6

; Sequence 6, Application US/09120601

; Patent No. 6207413

; GENERAL INFORMATION:

; APPLICANT: Masiaowski, Piotr

; TITLE OF INVENTION: No. 6207413el Orphan Receptors

; FILE REFERENCE: REG 630

; CURRENT APPLICATION NUMBER: US/09/120,601

; CURRENT FILING DATE: 1998-07-22

; EARLIER APPLICATION NUMBER: 09/012,072

; EARLIER FILING DATE: 1998-01-22

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 448

; TYPE: PRT

; ORGANISM: HUMAN

US-09-120-601-6

Query Match 92.2%; Score 2075.5; DB 2; Length 448;

Best Local Similarity 86.7%; Pred. No. 1.2e-185;

Matches 391; Conservative 5; Mismatches 14; Indels 41; Gaps 4;

QY 1 MPAGRPGPVAQARRPPRLSSLSWSPLLLCVLGPRGSGAHTAVISPDPTLLIGSSILQ 60

Db 1 MPAGRRGPAAQARRPP-PLLPL--LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLL 57

QY 61 ATCSIHGDPGATAEGLYTLNGRRLLPSBLRLLNTSTLALANLNGSRQSGDNLVCH 120

Db 58 ATCSVHGDPGATAEGLYTLNGRRLLPSBLRLLNTSTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKVKLRW 180

Db 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKVKLRW 177

Db 238 LPSPATPGLSLLVRGKVTTDPPPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIR 297

QY 279 YRVSDVDMKVVDDVSNQTSRCLAGLKPGTVYFVQVRCNPFYVGSKKAGIWSKSHPTA 338

Db 298 YRVSDVDMKVVDDVSNQTSRCLAGLKPGTVYFVQVRCNPFYVGSKKAGIWSKSHPTA 357

QY 339 ASTPRSERPGGVCBPRGSPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAMW 398

Db 358 ASTPRSERPGGVCBPRGSPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAMW 417

QY 399 QXSHKTRNQ-----VLPAKL 413

Db 418 QXSHKTRNQHRRTRGSCPRADGARREVLPDKL 448

RESULT 14

US-09-012-072-4

; Sequence 4, Application US/09012072

; Patent No. 6060276

; GENERAL INFORMATION:

; APPLICANT: Masiaowski, Piotr

; TITLE OF INVENTION: No. 6060276el Orphan Receptors

; FILE REFERENCE: REG 630

; CURRENT APPLICATION NUMBER: US/09/012,072

; CURRENT FILING DATE: 1998-01-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 434

; TYPE: PRT

; ORGANISM: HUMAN

US-09-012-072-4

Query Match 89.5%; Score 2015.5; DB 2; Length 434;

Best Local Similarity 86.7%; Pred. No. 4.9e-180;

Matches 379; Conservative 5; Mismatches 12; Indels 41; Gaps 4;

QY 15 RPPFLSSLSWSPLLLCVLGPRGSGAHTAVISPDPTLLIGSSILQATCSIHGDTFGATA 74

Db 1 RPP-PLLPL--LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSILATCSVHGDPGATA 57

QY 75 EGLYTLNGRRLLPSBLRLLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 134

Db 58 EGLYTLNGRRLLPSBLRLLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 117

QY 135 GLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKVKLRWYGODNTCEBYHTVG 194

Db 118 GLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKVKLRWYGODNTCEBYHTVG 177

QY 195 PHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDVLD----- 234

Db 178 PHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDVLDVSHLPLSPATPGLSLLVR 237

QY 235 --VTTDPPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDVDMKVVDD 292

Db 238 GRVTTDPPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDVDMKVVDD 297

QY 293 VSNQTSRCLAGLKPGTVYFVQVRCNPFYVGSKKAGIWSKSHPTAASTPRSERPGGVC 352

Db 298 VSNQTSRCLAGLKPGTVYFVQVRCNPFYVGSKKAGIWSKSHPTAASTPRSERPGGVC 357

QY 353 VCEPRGSGSPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ----- 407

Db 358 ACEPRGSGSPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ----- 417

QY 408 -----VLPAKL 413

Db 418 SCPRADGARREVLPDKL 434

RESULT 15

US-09-120-601-4

; Sequence 4, Application US/09120601

Tue Apr 11 10:57:44 2006

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; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-4

Query Match      89.5%; Score 2015.5; DB 2; Length 434;
Best Local Similarity 86.7%; Pred. No. 4.9e-180;
Matches 379; Conservative 5; Mismatches 12; Indels 41; Gaps 4;

Qy 15 RPPRLSSLSLLLCVLGVPRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATA 74
Db 1 RPP-FLPL--LLLCVLGAPRAGGAHTAVISPODPTLLIGSSLLATCSVHGDPGATA 57

Qy 75 EGLYWTNGRRRLPELSRLINTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 134
Db 58 EGLYWTNGRRRLPELSRLVNSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 117

Qy 135 GLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVG 194
Db 118 GLPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVG 177

Qy 195 PHSCHIPKDIALFTPYEIWVEATNRLGSARSVDLTLDVLD----- 234
Db 178 PHSCHIPKDIALFTPYEIWVEATNRLGSARSVDLTLDLDVGSHPPLSPATPGLSLIVR 237

Qy 235 --VTTTDPDPDVHVSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDD 292
Db 238 GKVVTTDPDPDVHVSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDD 297

Qy 293 VSNQTSCLAGLKP GTVYFVQVRCNPFYIGSKKAGIWSHPTAASPRSERPGPGG 352
Db 298 VSNQTSCLAGLKP GTVYFVQVRCNPFYIGSKKAGIWSHPTAASPRSERPGPGG 357

Qy 353 VCEPRGGEPSGPRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMKSHKTRNQ----- 407
Db 358 ACEPRGGEPSGPRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMKSHKTRNQRTRG 417

Qy 408 -----VLPAXL 413
Db 418 SCPRADGARREVLDPKL 434
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Search completed: April 11, 2006, 02:18:59  
Job time : 29.5393 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 02:36:34 ; Search time 96.1152 Seconds  
(without alignments)  
1795.383 Million cell updates/sec

Title: US-09-037-657-13

Perfect score: 2251

Sequence: 1 MPAGRPGVPAQSARPPRL.....WRAMQKSHKTRNQVLPAKL 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA\_Main:\*
- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*
  - 2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*
  - 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*
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  - 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2197.5	97.6	425	3	US-09-880-578-6
4	2119	94.1	407	4	US-10-247-463-5
5	2119	94.1	407	4	US-10-778-002-13
6	2119	94.1	407	5	US-10-777-789-13
7	2119	94.1	407	6	US-11-016-106-5
8	2118.5	94.1	405	3	US-09-736-842-2
9	2118.5	94.1	405	4	US-10-074-901-2
10	2114.5	93.9	410	4	US-10-247-463-4
11	2114.5	93.9	410	5	US-10-778-002-12
12	2114.5	93.9	410	5	US-10-777-789-12
13	2114.5	93.9	410	6	US-11-016-106-4
14	2098	93.2	425	3	US-09-880-578-4
15	2097.5	93.2	421	3	US-09-037-657-44
16	2096.5	93.1	426	4	US-10-056-984-2
17	2096.5	93.1	426	5	US-10-643-009-2
18	2096	93.1	422	3	US-09-866-028-32
19	2096	93.1	422	3	US-09-944-449-32
20	2096	93.1	422	3	US-09-944-457-32
21	2096	93.1	422	3	US-09-944-862-32
22	2096	93.1	422	3	US-09-945-587-32
23	2096	93.1	422	3	US-09-945-015-32
24	2096	93.1	422	3	US-09-944-396-32
25	2096	93.1	422	3	US-09-944-432-32
26	2096	93.1	422	3	US-09-943-762-32
27	2096	93.1	422	3	US-09-944-654-32

28	2096	93.1	422	3	US-09-943-851A-32	Sequence 32, Appl
29	2096	93.1	422	3	US-09-944-413-32	Sequence 32, Appl
30	2096	93.1	422	3	US-09-944-403-32	Sequence 32, Appl
31	2096	93.1	422	3	US-09-944-896-32	Sequence 32, Appl
32	2096	93.1	422	3	US-09-944-944-32	Sequence 32, Appl
33	2096	93.1	422	3	US-09-944-923-32	Sequence 32, Appl
34	2096	93.1	422	3	US-09-944-907-32	Sequence 32, Appl
35	2096	93.1	422	3	US-09-944-884-32	Sequence 32, Appl
36	2096	93.1	422	3	US-09-944-852-32	Sequence 32, Appl
37	2096	93.1	422	3	US-09-943-780-32	Sequence 32, Appl
38	2096	93.1	422	3	US-09-945-584-32	Sequence 32, Appl
39	2096	93.1	422	3	US-09-943-664-32	Sequence 32, Appl
40	2096	93.1	422	4	US-10-125-691-2	Sequence 2, Appl
41	2096	93.1	422	4	US-10-429-667-32	Sequence 32, Appl
42	2096	93.1	422	4	US-10-677-471-32	Sequence 32, Appl
43	2096	93.1	422	4	US-10-677-669-32	Sequence 32, Appl
44	2096	93.1	422	4	US-10-329-056-2	Sequence 2, Appl
45	2096	93.1	422	5	US-10-735-014-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-037-657-13  
; Sequence 13, Application US/09037657A  
; Patent No. US20020045741A1  
; GENERAL INFORMATION:  
; APPLICANT: Hilton, Douglas J.  
; APPLICANT: Nicola, Nicolas A.  
; APPLICANT: Farley, Allison  
; APPLICANT: Wilson, Tracy  
; APPLICANT: Zhang, Jian-Guo  
; APPLICANT: Alexander, Warren  
; APPLICANT: Rakar, Steven  
; APPLICANT: Fabri, Louis  
; APPLICANT: Kojima, Tetsuo  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Kikuchi, Yasufumi  
; APPLICANT: Nash, Andrew  
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
; FILE REFERENCE: DAVIES COLLISON CAVE (CIP)  
; CURRENT APPLICATION NUMBER: US/09/037,657A  
; CURRENT FILING DATE: 1998-03-10  
; EARLIER APPLICATION NUMBER: 08/928,720  
; EARLIER FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1  
US-09-037-657-13

Query Match	100.0%;	Score	2251;	DB 3;	Length	413;	
Best Local Similarity	100.0%;	Pred. No.	Se-166;				
Matches	413;	Conservative	0;	Mismatches	0;	Gaps	0;
Qy/	1	MPAGRPGVPAQSARRPRPLSSLSWSPULLLCVLGVPRGSGAHTAVISPODPTLLIGSSLQ	60				
Db	1	MPAGRPGVPAQSARRPRPLSSLSWSPULLLCVLGVPRGSGAHTAVISPODPTLLIGSSLQ	60				
Qy	61	ATCSIHGDTPGATAGELVYTLNGRRPLPSELSRLNTSTLALANLNGSRQSGDNLVCH	120				
Db	61	ATCSIHGDTPGATAGELVYTLNGRRPLPSELSRLNTSTLALANLNGSRQSGDNLVCH	120				
Qy	121	ARDGSILAGSCLVYGLPPEKPFNISCSWRNMKDLTCRWTPGAHGETFLHTNYSUKYKLRW	180				
Db	121	ARDGSILAGSCLVYGLPPEKPFNISCSWRNMKDLTCRWTPGAHGETFLHTNYSUKYKLRW	180				

QY 181 YGQDNTCEBYHTVGPBSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240  
DB 181 YGQDNTCEBYHTVGPBSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240  
QY 241 PPDVHVSRYGGLDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSNQTSR 300  
DB 241 PPDVHVSRYGGLDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSNQTSR 300  
QY 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360  
DB 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360  
QY 361 PSSGPVRRRLKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413  
DB 361 PSSGPVRRRLKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413

## RESULT 2

US-09-037-657-15  
; Sequence 15, Application US/09037657A  
; Patent No. US20020045741A1  
; GENERAL INFORMATION:  
; APPLICANT: Hilton, Douglas J.  
; APPLICANT: Nicola, Nicos A.  
; APPLICANT: Farley, Alison  
; APPLICANT: Wilson, Tracy  
; APPLICANT: Zhang, Jian-Guo  
; APPLICANT: Alexander, Warren  
; APPLICANT: Rakar, Steven  
; APPLICANT: Fabri, Louis  
; APPLICANT: Kojima, Tetsuo  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Kikuchi, Yasufumi  
; APPLICANT: Nash, Andrew  
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
; FILE REFERENCE: ENCODING SAME  
; CURRENT APPLICATION NUMBER: US/09/037,657A  
; CURRENT FILING DATE: 1998-03-10  
; EARLIER APPLICATION NUMBER: 08/928,720  
; EARLIER FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 425  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Murine NR6.2  
US-09-037-657-15

Query Match 98.9%; Score 2226.5; DB 3; Length 425;  
Best Local Similarity 98.8%; Pred. No. 4.1e-164;  
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;  
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DB 1 MPAGRPGVQAQARRPRPLSSLSWSPLLCLVGVPRGSGAHTAVISPODPTLLIGSSLQ 60  
QY 61 ATCSIHGDTFGTAEGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 61 ATCSIHGDTFGTAEGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120  
QY 121 ARDGSILAGSLYVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTYSLKYKLW 180  
DB 121 ARDGSILAGSLYVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTYSLKYKLW 180  
QY 181 YGQDNTCEBYHTVGPBSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240  
DB 181 YGQDNTCEBYHTVGPBSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240  
QY 241 PPDVHVSRYGGLDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSNQTSR 300

DB 241 PPDVHVSRYGGLDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSNQTSR 300  
QY 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360  
DB 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360  
QY 361 PSSGPVRRRLKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411  
DB 361 PSSGPVRRRLKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414

## RESULT 3

US-09-880-578-6  
; Sequence 6, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; Presnell, Scott R.  
; Jelmsberg, Anna C.  
; Gilbert, Teresa  
; Foster, Donald C.  
; Adams, Robyn L.  
; Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/09/880,578  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-880-578-6

Query Match 97.6%; Score 2197.5; DB 3; Length 425;  
Best Local Similarity 97.6%; Pred. No. 7.3e-162;  
Matches 404; Conservative 3; Mismatches 4; Indels 3; Gaps 1;  
QY 1 MPAGRPGVQAQARRPRPLSSLSWSPLLCLVGVPRGSGAHTAVISPODPTLLIGSSLQ 60  
DB 1 MPAGRPGVQAQARRPRPLSSLSWSPLLCLVGVPRGSGAHTAVISPODPTLLIGSSLH 60  
QY 61 ATCSIHGDTFGTAEGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120

Db 61 ATCSIHGDTGATAGLYWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCH 120  
QY 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
Db 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
QY 181 YGQDNTCEBYHTVGPCHPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 240  
Db 181 YGQDNTCEBYHTVGPCHPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 240  
QY 241 PPDVHVSRYGGLEDQLSVRWSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCKR 300  
Db 241 PPDVHVSRYGGLEDQLSVRWSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCKR 300  
QY 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGE 360  
Db 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGE 360  
QY 361 PSSGPVRRRLKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411  
Db 361 PSSGPVRRRLKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 414

## RESULT 4

US-10-247-463-5  
; Sequence 5, Application US/10247463  
; Publication No. US20030082734A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Lynette M.  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: DX0992Q  
; CURRENT APPLICATION NUMBER: US/10/247,463  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US/09/588,113  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: rodent  
US-10-247-463-5

Query Match 94.1%; Score 2119; DB 4; Length 407;  
Best Local Similarity 98.5%; Pred. No. 8.5e-156;  
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;  
QY 18 RPLSLWSPLLLCVIGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77  
Db 1 RPLSLWSPLLLCVIGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60  
QY 78 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 137  
Db 61 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 119  
QY 138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 197  
Db 120 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 179  
QY 198 CHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLS 257  
Db 180 CHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLS 239  
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCKRLAGLKPCTVYFVQVRCN 317  
Db 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCKRLAGLKPCTVYFVQVRCN 299  
QY 318 PFIYIGSKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGEPSGPPVRRRLKQFLGWL 377  
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

## RESULT 6

US-10-777-789-13  
; Sequence 13, Application US/10777789  
; Publication No. US20050048625A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando

Db 300 PFIYIGSKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGEPSGPPVRRRLKQFLGWL 359  
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411  
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

## RESULT 5

US-10-778-002-13  
; Sequence 13, Application US/10778002  
; Publication No. US20040192891A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/10/778,002  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/521,335  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: rodent  
US-10-778-002-13

Query Match 94.1%; Score 2119; DB 4; Length 407;  
Best Local Similarity 98.5%; Pred. No. 8.5e-156;  
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;  
QY 18 RPLSLWSPLLLCVIGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77  
Db 1 RPLSLWSPLLLCVIGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60  
QY 78 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 137  
Db 61 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 119  
QY 138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 197  
Db 120 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 179  
QY 198 CHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLS 257  
Db 180 CHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLS 239  
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCKRLAGLKPCTVYFVQVRCN 317  
Db 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCKRLAGLKPCTVYFVQVRCN 299  
QY 318 PFIYIGSKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGEPSGPPVRRRLKQFLGWL 377  
Db 300 PFIYIGSKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGEPSGPPVRRRLKQFLGWL 359  
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411  
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

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; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/10/777,789
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/521,335
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-10-777-789-13

Query Match          94.1%; Score 2119; DB 5; Length 407;
Best Local Similarity 98.5%; Pred. No. 8.5e-156;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY 18 RPLSLWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPGATAEGL 77
Db 1 RPLSLWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPGATAEGL 60

QY 78 YWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137
Db 61 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119

QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPHS 197
Db 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPHS 179

QY 198 CHIPKDALFTPEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 257
Db 180 CHIPKDALFTPEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 239

QY 258 VRWVSPPALKDFLFQAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 317
Db 240 VRWVSPPALKDFLFQAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 299

QY 318 PFGIYGSKKAGIWSWSHPTAASRPRPGGVCPRGCGPSSGPVRRRELKQFLGWL 377
Db 300 PFGIYGSKKAGIWSWSHPTAASRPRPGGVCPRGCGPSSGPVRRRELKQFLGWL 359

QY 378 KKHAYCSNLSFRLYDQWRAMQSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSFRLYDQWRAMQSHKTRNQDEGILPS 396

RESULT 7
US-11-016-106-5
; Sequence 5, Application US/11016106
; Publication No. US20050106673A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE REFERENCE: Methods
; CURRENT APPLICATION NUMBER: US/11/016,106
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-11-016-106-5

Query Match          94.1%; Score 2119; DB 6; Length 407;

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Best Local Similarity 98.5%; Pred. No. 8.5e-156;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY 18 RPLSLWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPGATAEGL 77
Db 1 RPLSLWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPGATAEGL 60

QY 78 YWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137
Db 61 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119

QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPHS 197
Db 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPHS 179

QY 198 CHIPKDALFTPEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 257
Db 180 CHIPKDALFTPEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 239

QY 258 VRWVSPPALKDFLFQAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 317
Db 240 VRWVSPPALKDFLFQAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 299

QY 318 PFGIYGSKKAGIWSWSHPTAASRPRPGGVCPRGCGPSSGPVRRRELKQFLGWL 377
Db 300 PFGIYGSKKAGIWSWSHPTAASRPRPGGVCPRGCGPSSGPVRRRELKQFLGWL 359

QY 378 KKHAYCSNLSFRLYDQWRAMQSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSFRLYDQWRAMQSHKTRNQDEGILPS 396

RESULT 8
US-09-736-842-2
; Sequence 2, Application US/09736842
; Publication No. US20030228653A1
; GENERAL INFORMATION:
; APPLICANT: Masiaowski, Piotr
; TITLE OF INVENTION: No. US20030228653A1el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-736-842-2

Query Match          94.1%; Score 2118.5; DB 3; Length 405;
Best Local Similarity 98.7%; Pred. No. 9.2e-156;
Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 21 SSLWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPGATAEGLYWT 80
Db 1 SSLWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTPGATAEGLYWT 60

QY 81 LNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 140
Db 61 LNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 120

QY 141 PFNISCWSNRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPHSCHI 200
Db 121 PFNISCWSNRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPHSCHI 180

QY 201 PKDALFTPEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLSVRW 260
Db 181 PKDALFTPEIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLSVRW 240

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QY 261 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQTYVYFVQVRCNPPG 320  
DB 241 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQTYVYFVQVRCNPPG 300  
QY 321 IYGSKAGIWSHSHPTASTPRSRPPGGVCGEPRGSGPVRRRLKQFLGWLKX 380  
DB 301 IYGSKAGIWSHSHPTASTPRSRPPGGVCGEPRGSGPVRRRLKQFLGWLKX 360  
QY 381 AYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411  
DB 361 AYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 394

## RESULT 9

US-10-074-901-2  
; Sequence 2, Application US/10074901  
; Publication No. US20020164785A1  
; GENERAL INFORMATION:  
; APPLICANT: Maslakowski, Piotr  
; TITLE OF INVENTION: No. US20020164785A1e1 Orphan Receptors  
; FILE REFERENCE: REG 630  
; CURRENT APPLICATION NUMBER: US/10/074,901  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US/09/012,072  
; PRIOR FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: MOUSE  
US-10-074-901-2

Query Match 94.1%; Score 2118.5; DB 4; Length 405;  
Best Local Similarity 98.7%; Pred. No. 9.2e-156;  
Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 21 SSLWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQATCSIHGDTPGATAGLYWT 80  
DB 1 SSLWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQATCSIHGDTPGATAGLYWT 60  
QY 81 LNRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 140  
DB 61 LNRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 120  
QY 141 PNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCBEYHTVGPCH 200  
DB 121 PNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCBEYHTVGPCH 180  
QY 201 PKDLALFTPYEIWEATNRLSGARSADVLTLDVLDVVTTPDPPDVHVSVRVGGLEDQLSVRW 260  
DB 181 PKDLALFTPYEIWEATNRLSGARSADVLTLDVLDVVTTPDPPDVHVSVRVGGLEDQLSVRW 240  
QY 261 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQTYVYFVQVRCNPPG 320  
DB 241 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQTYVYFVQVRCNPPG 300  
QY 321 IYGSKAGIWSHSHPTASTPRSRPPGGVCGEPRGSGPVRRRLKQFLGWLKX 380  
DB 301 IYGSKAGIWSHSHPTASTPRSRPPGGVCGEPRGSGPVRRRLKQFLGWLKX 360  
QY 381 AYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411  
DB 361 AYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 394

## RESULT 10

US-10-247-463-4  
; Sequence 4, Application US/10247463  
; Publication No. US20030082734A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Lynette M.

; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: DX09920  
; CURRENT APPLICATION NUMBER: US/10/247,463  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US/09/588,113  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate  
US-10-247-463-4

Query Match 93.9%; Score 2114.5; DB 4; Length 410;  
Best Local Similarity 94.7%; Pred. No. 1.9e-155;  
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRPGVAQSAARRPPRLSLWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQ 60  
DB 1 MPAGRPGVAQSAARRPPRLSLWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQ 57  
QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 58 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177  
QY 181 YQDNTCBEYHTVGPCHSKIPKDLALFTPYEIWEATNRLSGARSADVLTLDVLDVVTTP 240  
DB 178 YQDNTCBEYHTVGPCHSKIPKDLALFTPYEIWEATNRLSGARSADVLTLDVLDVVTTP 237  
QY 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
DB 238 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 297  
QY 301 LAGLKPQTYVYFVQVRCNPPGVIYGSKAGIWSHSHPTASTPRSRPPGGVCGEPRGSG 360  
DB 298 LAGLKPQTYVYFVQVRCNPPGVIYGSKAGIWSHSHPTASTPRSRPPGGVCGEPRGSG 357  
QY 361 PSSGVRRELKQFLGWLKXAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAK 413  
DB 358 PSSGVRRELKQFLGWLKXAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAK 410

## RESULT 11

US-10-778-002-12  
; Sequence 12, Application US/10778002  
; Publication No. US20040192891A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/10/778,002  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/521,335  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate

US-10-778-002-12

Query Match 93.9%; Score 2114.5; DB 4; Length 410;  
Best Local Similarity 94.7%; Pred. No. 1.9e-155;  
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGVPAQSAARRPPRLSSLSWPLLCVLGVRPGSGAHTAVISPODPTLLIGSSLLQ 60  
DB 1 MPAGRRGPAQAQARRPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57  
QY 61 ATCSIHGDTPGATAEGLYWTNGRLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 58 ATCSVHGDDPGATAEGLYWTNGRLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 180  
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 177

QY 181 YGQDNTCEYHTVGHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 240  
DB 178 YGQDNTCEYHTVGHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 237  
QY 241 PPDVHVSVRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300  
DB 238 PPDVHVSVRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 297  
QY 301 LAGLKPGTVYFVQVRCNPFYIYSGKKAGIWEWSHPTAASPRSRPGRGGVCEPRGGE 360  
DB 298 LAGLKPGTVYFVQVRCNPFYIYSGKKAGIWEWSHPTAASPRSRPGRGGVCEPRGGE 357  
QY 361 PSSGPVRRRELKQFLGWLKKGAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413  
DB 358 PSSGPVRRRELKQFLGWLKKGAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 410

RESULT 12

US-10-777-789-12  
; Sequence 12, Application US/10777789  
; Publication No. US20050048625A1  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/10/777,789  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/521,335  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate  
US-10-777-789-12

Query Match 93.9%; Score 2114.5; DB 5; Length 410;  
Best Local Similarity 94.7%; Pred. No. 1.9e-155;  
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGVPAQSAARRPPRLSSLSWPLLCVLGVRPGSGAHTAVISPODPTLLIGSSLLQ 60  
DB 1 MPAGRRGPAQAQARRPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57  
QY 61 ATCSIHGDTPGATAEGLYWTNGRLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 58 ATCSVHGDDPGATAEGLYWTNGRLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 180  
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 177

QY 181 YGQDNTCEYHTVGHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 240  
DB 178 YGQDNTCEYHTVGHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 237  
QY 241 PPDVHVSVRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300  
DB 238 PPDVHVSVRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 297  
QY 301 LAGLKPGTVYFVQVRCNPFYIYSGKKAGIWEWSHPTAASPRSRPGRGGVCEPRGGE 360  
DB 298 LAGLKPGTVYFVQVRCNPFYIYSGKKAGIWEWSHPTAASPRSRPGRGGVCEPRGGE 357  
QY 361 PSSGPVRRRELKQFLGWLKKGAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413  
DB 358 PSSGPVRRRELKQFLGWLKKGAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 410

RESULT 13

US-11-016-106-4  
; Sequence 4, Application US/11016106  
; Publication No. US20050106673A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Lynette M.  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: DX0992Q  
; CURRENT APPLICATION NUMBER: US/11/016,106  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate  
US-11-016-106-4

Query Match 93.9%; Score 2114.5; DB 6; Length 410;  
Best Local Similarity 94.7%; Pred. No. 1.9e-155;  
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGVPAQSAARRPPRLSSLSWPLLCVLGVRPGSGAHTAVISPODPTLLIGSSLLQ 60  
DB 1 MPAGRRGPAQAQARRPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57  
QY 61 ATCSIHGDTPGATAEGLYWTNGRLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 58 ATCSVHGDDPGATAEGLYWTNGRLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 180  
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 177  
QY 181 YGQDNTCEYHTVGHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 240  
DB 178 YGQDNTCEYHTVGHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLDVLDVTTDP 237  
QY 241 PPDVHVSVRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300  
DB 238 PPDVHVSVRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 297  
QY 301 LAGLKPGTVYFVQVRCNPFYIYSGKKAGIWEWSHPTAASPRSRPGRGGVCEPRGGE 360  
DB 298 LAGLKPGTVYFVQVRCNPFYIYSGKKAGIWEWSHPTAASPRSRPGRGGVCEPRGGE 357  
QY 361 PSSGPVRRRELKQFLGWLKKGAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413

Db 358 PSSGPRVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410

RESULT 14  
US-09-880-578-4  
; Sequence 4, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; Presnell, Scott R.  
; Jelmsberg, Anna C.  
; Gilbert, Teresa  
; Foster, Donald C.  
; Adams, Robyn L.  
; Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/880,578  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-880-578-4

Query Match 93.2%; Score 2098; DB 3; Length 425;  
Best Local Similarity 91.1%; Pred. No. 3.8e-154;  
Matches 391; Conservative 5; Mismatches 13; Indels 20; Gaps 3;  
QY 1 MPAGRPGVQAQARRPPRLSSLSWSPLLLCVLGVRGSGAHTAVISPDPTLLIGSSSQ 60  
Db 1 MPAGRPGVQAQARRPP-PLLP-LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLL 56  
QY 61 ATCSIHGDTPGATAGLYTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
Db 57 ATCSVHGDPFGATAGLYTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 116  
QY 121 ARDGSILAGSCLVGLPPEKPNISCSWKNMKTLCRWTPGAGHETFLHTNYSKYLKW 180  
Db 117 ARDGSILAGSCLVGLPPEKPNISCSWKNMKTLCRWTPGAGHETFLHTNYSKYLKW 176  
QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTDP 240

Db 177 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTDP 236  
QY 241 PPDVHVSRYGGLDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDKVVDVDSNOTSCR 300  
Db 237 PPDVHVSRYGGLDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDKVVDVDSNOTSCR 296  
QY 301 LAGLKPGTVYFQVRCNPFYIYSGKAGIWSWSHPTAASTPRSERPGPGGGVCEPRGGE 360  
Db 297 LAGLKPGTVYFQVRCNPFYIYSGKAGIWSWSHPTAASTPRSERPGPGGGVCEPRGGE 356  
QY 361 PSSGPRVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----- 407  
Db 357 PSSGPRVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQSPRADGA 416  
QY 408 ---VLPKAL 413  
Db 417 RREVLPDKL 425

RESULT 15  
US-09-037-657-44  
; Sequence 44, Application US/09037657A  
; Patent No. US20020045741A1  
; GENERAL INFORMATION:  
; APPLICANT: Hilton, Douglas J.  
; APPLICANT: Nicola, Nicos A.  
; APPLICANT: Farley, Alison  
; APPLICANT: Wilson, Tracy  
; APPLICANT: Zhang, Jian-Guo  
; APPLICANT: Alexander, Warren  
; APPLICANT: Rakar, Steven  
; APPLICANT: Fabri, Louis  
; APPLICANT: Kojima, Tetsuo  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Kikuchi, Yasufumi  
; APPLICANT: Nash, Andrew  
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
; FILE REFERENCE: DAVIES COLLISON CAVE (CIP)  
; CURRENT APPLICATION NUMBER: US/09/037,657A  
; CURRENT FILING DATE: 1998-03-10  
; EARLIER APPLICATION NUMBER: 08/928,720  
; EARLIER FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Amino Acid Sequence of NR6  
US-09-037-657-44

Query Match 93.2%; Score 2097.5; DB 3; Length 421;  
Best Local Similarity 93.7%; Pred. No. 4.1e-154;  
Matches 388; Conservative 7; Mismatches 12; Indels 7; Gaps 3;  
QY 1 MPAGRPGVQAQARRPPRLSSLSWSPLLLCVLGVRGSGAHTAVISPDPTLLIGSSSQ 60  
Db 1 MPAGRPGVQAQARRPP-PLLP-LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLL 56  
QY 61 ATCSIHGDTPGATAGLYTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
Db 57 ATCSVHGDPFGATAGLYTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 116  
QY 121 ARDGSILAGSCLVGLPPEKPNISCSWKNMKTLCRWTPGAGHETFLHTNYSKYLKW 180  
Db 117 ARDGSILAGSCLVGLPPEKPNISCSWKNMKTLCRWTPGAGHETFLHTNYSKYLKW 176  
QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTDP 240  
Db 177 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTDP 236

Qy	241	PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR	300
Db	237	PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR	296
Qy	301	LAGLXPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGGE	360
Db	297	LAGLXPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGGGGACERGGE	356
Qy	361	PSSGPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ---	411
Db	357	PSSGPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS	410

Search completed: April 11, 2006, 02:43:00  
Job time : 97.1152 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 02:03:38 ; Search time 116.124 Seconds  
(without alignments)  
1608.075 Million cell updates/sec

Title: US-09-037-657-15

Perfect score: 2317

Sequence: 1 MPAGRPGVQAQSRAPRPL.....NODEGILPSGRGAARGPAG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2317	100.0	425	2 AAW55012	Novel hae
2	2317	100.0	425	3 AAY93659	Novel hae
3	2317	100.0	425	4 AAE00821	Novel hae
4	2313	99.8	425	2 AAW59804	Nucleotid
5	2313	99.8	425	2 AAY26337	Murine U4
6	2288	98.7	425	2 AAW70862	Rat Zcyto
7	2226.5	96.1	413	2 AAW55011	Novel hae
8	2226.5	96.1	413	3 AAY93658	A murine
9	2226.5	96.1	413	4 AAE00820	Murine ha
10	2225	96.0	416	2 AAY29780	Mouse DNA
11	2209.5	95.4	407	3 AAB19589	Mouse cyt
12	2209.5	95.4	407	4 AAB36648	Mouse cyt
13	2209.5	95.4	407	7 ADC07180	Mouse cyt
14	2209.5	95.4	407	8 ADT90845	Mouse cyt
15	2209.5	95.4	407	8 ADT61033	Mouse cyt
16	2209.5	95.4	407	9 ADY57158	Mouse cyt
17	2209.5	95.4	407	9 ADZ65015	Mouse NR6
18	2209	95.3	405	2 AAY15214	Amino aci
19	2209	95.3	405	3 AAY44839	Mouse orp
20	2178	94.0	421	4 AAE00826	Murine ha
21	2176.5	93.9	422	2 AAY05782	Human typ
22	2176.5	93.9	422	2 AAY06479	Human typ
23	2176.5	93.9	422	2 AAY17825	Human PRO
24	2176.5	93.9	422	2 AAY26339	Human U4

25	2176.5	93.9	422	3 AAB01316	Human PRO
26	2176.5	93.9	422	3 AAY93686	Amino aci
27	2176.5	93.9	422	4 AAG63545	Amino aci
28	2176.5	93.9	422	6 ABUS5925	Human sec
29	2176.5	93.9	422	6 ABUS5925	Human sec
30	2176.5	93.9	422	6 ABUS5925	Human sec
31	2176.5	93.9	422	6 ABUS5925	Human sec
32	2176.5	93.9	422	6 ABUS5925	Human sec
33	2176.5	93.9	422	6 ABUS5925	Human sec
34	2176.5	93.9	422	6 ABUS5925	Human sec
35	2176.5	93.9	422	6 ABUS5925	Human sec
36	2176.5	93.9	422	6 ABUS5925	Human sec
37	2176.5	93.9	422	6 ABUS5925	Human sec
38	2176.5	93.9	422	7 ADC25788	Human sec
39	2176.5	93.9	422	7 ADC25788	Human sec
40	2176.5	93.9	422	7 ADC25788	Human sec
41	2176.5	93.9	422	7 ADC25788	Human sec
42	2176.5	93.9	422	8 ADE71501	Human sec
43	2176.5	93.9	422	8 ADG63444	Human sec
44	2176.5	93.9	422	8 ADH43173	Human sec
45	2176.5	93.9	422	8 ADN04232	Antipsori

#### ALIGNMENTS

##### RESULT 1

AAW55012

ID AAW55012 standard; protein; 425 AA.

XX AC AAW55012;

XX DT 29-SEP-1998 (first entry)

XX DE Novel haemopoietin receptor NR6.2 protein.

XX KW Haemopoietin receptor; cell proliferation; cancer;

XX KW cell survival; therapeutic; neuronal proliferation; drug screening;

XX KW Mouse.

XX OS Mus sp.

XX PN WO9811225-A2.

XX PD 19-MAR-1998.

XX PF 11-SEP-1997; 97WO-GB002479.

XX PR 11-SEP-1996; 96AU-00002246.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX (DZIE/) DZIEGLEWSKA H E.

XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;

XX Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;

XX WPI: 1998-260970/23.

XX N-PSDB; AAV27141.

XX New isolated haemopoietin receptor - used for developing products for

XX modulating proliferation, differentiation and survival of cells, e.g.

XX neuronal cells.

XX Claim 15; Page 84-87; 182pp; English.

XX The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.

XX Interaction between the novel HR and a ligand facilitates proliferation,

XX differentiation and survival of a wide variety of cells. The HR and it's

XX derivatives can be used for modulating the activity of the receptors e.g.

XX to regulate development, maintenance or regeneration in an array of

XX different cells and tissues in vitro and in vivo. They can be present in

XX therapeutics used for modulating neuronal proliferation, differentiation

XX and survival. The products can also be used for detection and diagnosis,

CC e.g. for cancers or predisposition to cancers, or for drug screening  
 XX  
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2317; DB 2; Length 425;  
 Best Local Similarity 100.0%; Pred. No. 8e-193;  
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGVVAQSARRPPRLSSLSWSPDLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60  
 DB 1 MPAGRPGVVAQSARRPPRLSSLSWSPDLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 240  
 DB 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 240

QY 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300

QY 301 LAGLKPCTVYFVQVRCNPFYIYVGSKAGIWSWSHPTAASRPRSGPGGGVCEPRGGE 360  
 DB 301 LAGLKPCTVYFVQVRCNPFYIYVGSKAGIWSWSHPTAASRPRSGPGGGVCEPRGGE 360

QY 361 PSSGPVRRRELKQFLGWLKKGHCNSLSPRLYDQWRAWMQKSHKTRNQDSGILPSSGRGAA 420  
 DB 361 PSSGPVRRRELKQFLGWLKKGHCNSLSPRLYDQWRAWMQKSHKTRNQDSGILPSSGRGAA 420

QY 421 RGPAG 425  
 DB 421 RGPAG 425

RESULT 2  
 AAY93659  
 ID AAY93659 standard; protein; 425 AA.  
 AC AAY93659;  
 XX  
 XX 25-SEP-2000 (first entry)  
 DT  
 DE A murine hemopoietin receptor NR6.2 polypeptide.  
 XX  
 XX Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;  
 KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;  
 KW suckling; postnatal baby; foetal testing.  
 XX  
 XX Mus musculus.  
 XX  
 XX WO200035471-A1.  
 PN  
 PD 22-JUN-2000.  
 XX  
 XX 17-DEC-1999; 99WO-AU001119.  
 XX  
 XX 17-DEC-1998; 98AU-00007762.  
 PR  
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
 PA  
 XX Alexander WS, Metcalf D;  
 PI  
 XX WFI; 2000-442273/38.  
 DR  
 XX N-PSDB; AAA46792.  
 XX  
 XX Administering the hemopoietin receptor NR6 is used to modulate production

PT of hemopoietic progenitor cells and facilitate postnatal survival of  
 PT mammals by inducing or promoting suckling.  
 XX  
 PS Claim 5; Page 73-74; 77pp; English.  
 XX  
 CC The present sequence represents a murine haemopoietin receptor NR6 (CLF-  
 CC 1) polypeptide. The specification describes a method for the treatment or  
 CC prophylaxis of disease conditions associated with dysfunctional  
 CC haemopoietic regulation. The method comprises modulating the production  
 CC of hemopoietic progenitor cells in a mammal by administering the product  
 CC of decreasing production of progenitor cells may be used in the treatment of  
 CC cancer or to induce apoptosis of particular cell types. Increasing  
 CC production of progenitor cells is used to facilitate postnatal survival  
 CC in mammals by inducing or promoting suckling. Potential disease  
 CC conditions may be identified by monitoring NR6 production in postnatal  
 CC babies or allowing expectant mothers to undergo foetal testing. Low NR6  
 CC levels can then be treated immediately  
 XX  
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2317; DB 3; Length 425;  
 Best Local Similarity 100.0%; Pred. No. 8e-193;  
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGVVAQSARRPPRLSSLSWSPDLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60  
 DB 1 MPAGRPGVVAQSARRPPRLSSLSWSPDLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 240  
 DB 181 YQDNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 240

QY 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300

QY 301 LAGLKPCTVYFVQVRCNPFYIYVGSKAGIWSWSHPTAASRPRSGPGGGVCEPRGGE 360  
 DB 301 LAGLKPCTVYFVQVRCNPFYIYVGSKAGIWSWSHPTAASRPRSGPGGGVCEPRGGE 360

QY 361 PSSGPVRRRELKQFLGWLKKGHCNSLSPRLYDQWRAWMQKSHKTRNQDSGILPSSGRGAA 420  
 DB 361 PSSGPVRRRELKQFLGWLKKGHCNSLSPRLYDQWRAWMQKSHKTRNQDSGILPSSGRGAA 420

QY 421 RGPAG 425  
 DB 421 RGPAG 425

RESULT 3  
 AAE00821  
 ID AAE00821 standard; protein; 425 AA.  
 AC AAE00821;  
 XX  
 XX 09-SEP-2004 (revised)  
 DT 02-JUL-2001 (first entry)  
 XX  
 XX Murine haemopoietin receptor, NR6.2 isoform.  
 DE  
 XX Murine; biologically active complex; haemopoietin receptor; NR6;  
 KW cardiotrophic-like cytokine; CLC; therapy; prophylaxis; proliferation;  
 KW differentiation; cell survival; neurotrophic activity.  
 XX  
 XX Mus sp.



Db 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDVLTLDVLDVVTDP 240  
Qy 241 PPDVHVSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKWVDDVSNQTSR 300  
Db 241 PPDVHVSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKWVDDVSNQTSR 300  
Qy 301 LAGLKPGTVYFVQVRCNPFGIYGSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
Db 301 LAGLKPGTVYFVQVRCNPFGIYGSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
Qy 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSSRRGAA 420  
Db 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSSRRGAA 420  
Qy 421 RGPAG 425  
Db 421 RGPAG 425

RESULT 5  
AAV26337  
ID AAV26337 standard; protein; 425 AA.  
XX AAY26337;  
DT 13-JAN-2000 (first entry)  
DE Murine U4 haematopoietin receptor superfamily chain.  
XX  
KW Murine U4 protein; haematopoietin receptor superfamily;  
KW biological activity; cytokine; cell proliferation; cell differentiation;  
KW immune stimulation; immune suppression; haematopoiesis regulation;  
KW immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;  
KW myeloid cell; lymphoid cell deficiency; platelet disorder.  
OS Mus sp.

Key Location/Qualifiers  
FT Peptide 1..40  
FT Protein /label= Putative\_signal\_sequence  
FT /label= Mature\_murine\_U4  
XX WO9953066-A1.  
XX 21-OCT-1999.  
XX 09-APR-1999; 99WO-US007882.  
XX 10-APR-1998; 98US-00058660.  
XX (GEMV ) GENETICS INST INC.  
XX Donaldson D, Collins M, Whitters M, Neben T;  
XX WPI; 1999-611303/52.  
XX N-PSDB; AAX90752.  
XX Novel polypeptides and polynucleotides used for treatment of human  
XX diseases and disorders e.g. immune disorders or deficiencies caused by  
XX fungal, parasitic or viral infections.  
XX Claim 9; Page 31-32; 43pp; English.  
XX The present sequence is a murine U4 protein which is a member of  
XX haematopoietin receptor superfamily. The protein sequence has conserved  
XX cysteine pairs and WSXWS motifs characteristic of the receptor family. It  
XX is predicted to have the following biological activities: cytokine, cell  
XX proliferation/differentiation, immune stimulating or suppressing and  
XX haematopoiesis regulating. The U4 protein can be used to treat immune  
XX disorders and deficiencies, autoimmune disorders, allergies, cancer,  
XX myeloid or lymphoid cell deficiencies and platelet disorders

XX Sequence 425 AA;  
SQ Query Match 99.8%; Score 2313; DB 2; Length 425;  
Best Local Similarity 99.8%; Pred. No. 1.8e-192;  
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MPAGRPGVAQSARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSILQ 60  
Db 1 MPAGRPGVAQSARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSILQ 60  
Qy 61 ATCSIHGDTPTGATAGELYWTINGRRLPSELGRLLNTSTLALANLINGSRQOSGDNLVCH 120  
Db 61 ATCSIHGDTPTGATAGELYWTINGRRLPSELGRLLNTSTLALANLINGSRQOSGDNLVCH 120  
Qy 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180  
Db 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180  
Qy 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDVLTLDVLDVVTDP 240  
Db 181 YGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDVLTLDVLDVVTDP 240  
Qy 241 PPDVHVSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKWVDDVSNQTSR 300  
Db 241 PPDVHVSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKWVDDVSNQTSR 300  
Qy 301 LAGLKPGTVYFVQVRCNPFGIYGSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
Db 301 LAGLKPGTVYFVQVRCNPFGIYGSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360  
Qy 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSSRRGAA 420  
Db 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSSRRGAA 420  
Qy 421 RGPAG 425  
Db 421 RGPAG 425  
RESULT 6  
AAW70862  
ID AAW70862 standard; protein; 425 AA.  
XX AAW70862;  
XX 17-MAR-1999 (first entry)  
XX DE Rat Zcytor5 protein.  
XX Zcytor5; cytokinin-like receptor; down-regulation; growth factor;  
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;  
KW cardiac pathology; heart enlargement; Zcytor5 ligand.  
XX Rattus sp.  
XX WO9849307-A1.  
XX 05-NOV-1998.  
XX 01-MAY-1998; 98WO-US008865.  
XX 01-MAY-1997; 97US-0045287P.  
XX 01-MAY-1997; 97US-00850030.  
XX 13-FEB-1998; 98US-00023890.  
XX 13-FEB-1998; 98US-0074721P.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX PA Lok S, Presnell SR, Jelmsberg AC, Gilbert T, Whitmore TB;  
XX PI Foster DC, Adams RL, Lehner JW;  
XX WPI; 1999-034662/03.  
DR

DR N-PSDB; AAU70896.  
 XX New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-  
 PT regulating Zcytor5 natural ligands or detecting cardiotrophin-1 in blood.  
 XX  
 XX Claim 1; Page 75-76; 55pp; English.

CC The present sequence represents a protein designated Zcytor5, which is a  
 CC cytokinin-like receptor. Soluble Zcytors may be administered to down-  
 CC regulate the effects of a growth and/or maintenance factor in thyroid,  
 CC heart, and skeletal muscle for example to lessen the effect of  
 CC cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement.  
 CC Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to  
 CC discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA  
 CC or RNA can be used to determine the presence and integrity of the Zcytor5  
 CC gene on chromosome 19. Antibodies and the anti-idiotypic antibody could  
 CC be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand  
 CC effects

XX Sequence 425 AA;

Query Match 98.7%; Score 2288; DB 2; Length 425;  
 Best Local Similarity 98.8%; Pred. No. 2.7e-190; Mismatches 4; Indels 0; Gaps 0;  
 Matches 420; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MPAGRPGVPAQSARPPRLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSIQ 60  
 DB 1 MPAGRPGVPAQSARPPRLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSIQ 60  
 QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 DB 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 QY 181 YQDNTCEYHTVGPCHSCHIPKDLPALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240  
 DB 181 YQDNTCEYHTVGPCHSCHIPKDLPALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240  
 QY 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSR 300  
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSR 300  
 QY 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360  
 DB 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360  
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSSRRGAA 420  
 DB 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSSRRGAA 420  
 QY 421 RGPAG 425  
 DB 421 RGPAG 425

RESULT 7

AAW5011  
 ID AAW5011 standard; protein; 413 AA.

XX AAW5011;

XX 29-SEP-1998 (first entry)

DE Novel haemopoietin receptor NR6.1 protein.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;  
 KW cell survival; therapeutic; neuronal proliferation; drug screening;  
 KW Mouse.

OS Mus sp.

XX WO9811225-A2.

XX 19-MAR-1998.

XX 11-SEP-1997; 97WO-GB002479.

XX 11-SEP-1996; 96AU-00002246.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
 XX (DZIE/) DZIELEWSKA H E.

XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;  
 XX Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;

XX WPI: 1998-260970/23.

XX N-PSDB; AAU27140.

XX New isolated haemopoietin receptor - used for developing products for  
 PT modulating proliferation, differentiation and survival of cells, e.g.  
 PT neuronal cells.

XX Claim 14; Page 77-81; 182pp; English.

XX The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.  
 CC Interaction between the novel HR and a ligand facilitates proliferation,  
 CC differentiation and survival of a wide variety of cells. The HR and it's  
 CC derivatives can be used for modulating the activity of the receptors e.g.  
 CC to regulate development, maintenance or regeneration in an array of  
 CC different cells and tissues in vitro and in vivo. They can be present in  
 CC therapeutics used for modulating neuronal proliferation, differentiation  
 CC and survival. The products can also be used for detection and diagnosis,  
 CC e.g. for cancers or predisposition to cancers, or for drug screening

XX Sequence 413 AA;

Query Match 96.1%; Score 2226.5; DB 2; Length 413;  
 Best Local Similarity 98.8%; Pred. No. 5.9e-185;  
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRPGVPAQSARPPRLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSIQ 60

DB 1 MPAGRPGVPAQSARPPRLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSIQ 60

QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

DB 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPCHSCHIPKDLPALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240

DB 181 YQDNTCEYHTVGPCHSCHIPKDLPALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240

QY 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSR 300

DB 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSR 300

QY 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360

DB 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360

QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

DB 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 8

AAU93658

ID AAU93658 standard; protein; 413 AA.

XX

AC AAY93658;  
XX 25-SEP-2000 (first entry)  
XX A murine hemopoietin receptor NR6.1 polypeptide.  
DE Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;  
KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;  
KW suckling; postnatal baby; foetal testing.  
XX Mus musculus.  
XX WO200035471-A1.  
XX 22-JUN-2000.  
XX 17-DEC-1999; 99WO-AU001119.  
XX 17-DEC-1998; 98AU-00007762.  
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX Alexander WS, Metcalf D;  
XX WPI; 2000-442273/38.  
XX N-PSDB; AAA46791.  
XX Administering the hemopoietin receptor NR6 is used to modulate production  
XX of hemopoietic progenitor cells and facilitate postnatal survival of  
XX mammals by inducing or promoting suckling.  
XX Claim 5; Page 70-71; 77pp; English.  
XX The present sequence represents a murine haemopoietin receptor NR6 (CLF-  
CC 1) polypeptide. The specification describes a method for the treatment or  
CC prophylaxis of disease conditions associated with dysfunctional  
CC haemopoietic regulation. The method comprises modulating the production  
CC of hemopoietic progenitor cells in a mammal by administration of NR6.  
CC Decreasing production of progenitor cells may be used in the treatment of  
CC cancer or to induce apoptosis of particular cell types. Increasing  
CC production of progenitor cells is used to facilitate postnatal survival  
CC in mammals by inducing or promoting suckling. Potential disease  
CC conditions may be identified by monitoring NR6 production in postnatal  
CC babies or allowing expectant mothers to undergo foetal testing. Low NR6  
CC levels can then be treated immediately  
XX Sequence 413 AA;  
Query Match 96.1%; Score 2226.5; DB 3; Length 413;  
Best Local Similarity 98.8%; Pred. No. 5.9e-185;  
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;  
QY 1 MPAGRPGVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGGGAHTAVISPODPTLLIGSSLQ 60  
DB 1 MPAGRPGVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGGGAHTAVISPODPTLLIGSSLQ 60  
QY 61 ATCSIHGDTFGAETAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 61 ATCSIHGDTFGAETAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAGETFLHTNYSKYKLW 180  
DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAGETFLHTNYSKYKLW 180  
QY 181 YGDNNTCEEVHTVGRHSCHIPKDALFTPEIWEATNRLGSARSDVLTDLVDVTTDP 240  
DB 181 YGDNNTCEEVHTVGRHSCHIPKDALFTPEIWEATNRLGSARSDVLTDLVDVTTDP 240  
QY 241 PPDVHVSVRGLEDQLSVRWVSPALKDQFLQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
DB 241 PPDVHVSVRGLEDQLSVRWVSPALKDQFLQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
QY 301 LAGLKPQGVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASRPRPFGGVCERGG 360

DB 301 LAGLKPQGVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASRPRPFGGVCERGG 360  
QY 361 PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQSHKTRNQDGLIPS 414  
DB 361 PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQSHKTRNQ---VLPA 411  
RESULT 9  
AAE00820  
ID AAE00820 standard; protein; 413 AA.  
XX AAE00820;  
XX 09-SEP-2004 (revised)  
DT 02-JUL-2001 (first entry)  
XX Murine haemopoietin receptor, NR6.1 isoform.  
XX Murine; biologically active complex; haemopoietin receptor; NR6;  
KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;  
KW differentiation; cell survival; neurotrophic activity.  
XX Mus sp.  
XX Unidentified.  
XX Key Location/Qualifiers  
FH Domain 330..334  
FT /label = WSXWS\_motif  
XX WO200127157-A1.  
XX 19-APR-2001.  
XX 06-OCT-2000; 2000WO-AU001216.  
XX 08-OCT-1999; 99AU-00003327.  
PR 12-MAY-2000; 2000AU-00007489.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;  
PI Nakata Y, Hasegawa M;  
XX WPI; 2001-281978/29.  
DR N-PSDB; AAD04192.  
XX New biologically active complex comprising NR6 and cardiotrophin-like-  
PT cytokine, for facilitating proliferation, differentiation and/or survival  
PT of a cell.  
XX Claim 25; Page 76-77; 123pp; English.  
XX The present invention relates to a biologically active complex comprising  
CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The  
CC complex is useful in the manufacture of a medicament for the treatment  
CC and/or prophylaxis of a subject, as it is involved in facilitating  
CC proliferation, differentiation and/or survival of a cell. The complex or  
CC its components have neurotrophic activity. The present sequence is murine  
CC haemopoietin receptor, NR6.1 isoform. The NR6.1 represents the NR6 splice  
CC variant obtained due to alternative mRNA splicing  
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key  
XX Sequence 413 AA;  
Query Match 96.1%; Score 2226.5; DB 4; Length 413;  
Best Local Similarity 98.8%; Pred. No. 5.9e-185;  
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;  
QY 1 MPAGRPGVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGGGAHTAVISPODPTLLIGSSLQ 60  
DB 1 MPAGRPGVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGGGAHTAVISPODPTLLIGSSLQ 60

QY 61 ATCSIHGDTGATAEGLYWTNGRRPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 |||||  
 Db 61 ATCSIHGDTGATAEGLYWTNGRRPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
 |||||  
 QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKW 180  
 |||||  
 Db 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKW 180  
 |||||  
 QY 181 YGQDNTCEEYHTVGPSPHCHIPKDLALFTPYEIVWEATNRLGARSVDVLTDLVDLVTTDP 240  
 |||||  
 Db 181 YGQDNTCEEYHTVGPSPHCHIPKDLALFTPYEIVWEATNRLGARSVDVLTDLVDLVTTDP 240  
 |||||  
 QY 241 PPDVHVSRLVGLDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSR 300  
 |||||  
 Db 241 PPDVHVSRLVGLDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSR 300  
 |||||  
 QY 301 LAGLKPGTVVYFVQVRCNPFPGIYSGKKAGIWESEHPTAASTPRSRPGGGVCEPRGGE 360  
 |||||  
 Db 301 LAGLKPGTVVYFVQVRCNPFPGIYSGKKAGIWESEHPTAASTPRSRPGGGVCEPRGGE 360  
 |||||  
 QY 361 PSSGPPVRLRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414  
 |||||  
 Db 361 PSSGPPVRLRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411  
 |||||

## RESULT 10

AAV29780

ID AAV29780 standard; protein; 416 AA.

XX

AC AAV29780;

XX

DT 04-NOV-1999 (first entry)

XX

DE Mouse DNAX soluble receptor subunit 1.

XX

KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 interleukin B30; DSRs1; IL-B30; cytokine receptor; diagnosis;  
 inflammatory disorder; inflammatory response; innate immunity;  
 morphogenic development; immunological disorder.

XX

OS Mus sp.

XX

PN WO9940195-A1.

XX

PD 12-AUG-1999.

XX

PF 05-FEB-1999; 99WO-US002600.

XX

PR 06-FEB-1998; 98US-0073941P.

XX

PR 13-MAY-1998; 98US-00078194.

XX

PA (SCHE ) SCHERING CORP.

XX

PI Mattson JD, Mcclanahan TK, Kastelein RA;

XX

DR WPI; 1999-527306/44.

XX

DR N-PSDB; AA208862.

XX

PT New receptor subunits useful in the treatment inflammatory disorders.

XX

PS Claim 2; Page 24-25; 133pp; English.

XX

CC The present invention describes a composition (I) comprising DNAX  
 cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 subunit I (DSRS1) protein, which together encode a new mammalian cytokine  
 -related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or  
 DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRS1 is useful for  
 screening for ligands (i.e. agonists/antagonists) from a library of  
 compounds, which are useful for modulating the physiology or development  
 of a cell or tissue culture e.g. inflammatory responses, innate immunity  
 and/or morphogenic development. (R), antibodies and ligands are useful  
 for treatment of conditions, especially immunological disorders,

CC

CC associated with conditions exhibiting abnormal expression of (R). (R) is  
 useful as a phosphate labeling enzyme to label substrates, and the  
 subunits DSRs1 and DCRS1 are useful as immunogens for generating  
 antibodies, or as antigens for binding antibodies. Nucleic acids encoding  
 (R) are useful for identifying related DNAs and mRNAs, and variants from  
 other individuals or species. The present sequence represents the  
 specifically claimed mouse DSRs1, for use in the composition of the  
 present invention

XX  
 SQ Sequence 416 AA;

Query Match 96.0%; Score 2225; DB 2; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 8e-185;  
 Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RPLSSLSWSPLLLCVLGVPGRGGGAHTAVISPOPTLLIGSSLOATCSIHGDTPGATAEGL 77  
 |||||  
 Db 9 RPLSSLSWSPLLLCVLGVPGRGGGAHTAVISPOPTLLIGSSLOATCSIHGDTPGATAEGL 68  
 |||||  
 QY 78 YWTNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLVYGLP 137  
 |||||  
 Db 69 YWTNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLVYGLP 128  
 |||||  
 QY 138 PEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGP 197  
 |||||  
 Db 129 PEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGP 188  
 |||||  
 QY 198 CHIPKDLALFTPYEIVWEATNRLGARSVDVLTDLVDLVTTDPDPVHVSRLVGLDQLS 257  
 |||||  
 Db 189 CHIPKDLALFTPYEIVWEATNRLGARSVDVLTDLVDLVTTDPDPVHVSRLVGLDQLS 248  
 |||||  
 QY 258 VRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSCLAGLKPGTVVYFVQVRCN 317  
 |||||  
 Db 249 VRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSCLAGLKPGTVVYFVQVRCN 308  
 |||||  
 QY 318 PFGIYSGKKAGIWESEHPTAASTPRSRPGGGVCEPRGSGPVRRELKQFLGWL 377  
 |||||  
 Db 309 PFGIYSGKKAGIWESEHPTAASTPRSRPGGGVCEPRGSGPVRRELKQFLGWL 368  
 |||||  
 QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGAARGPAG 425  
 |||||  
 Db 369 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGAARGPAG 416  
 |||||

## RESULT 11

AAB19589

ID AAB19589 standard; protein; 407 AA.

XX

AC AAB19589;

XX

DT 22-JAN-2001 (first entry)

XX

DE Mouse cytokine-like factor-1.

XX

KW Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; mouse; cytokine;  
 receptor; neuron; inflammation; antiinflammatory; autoimmune disease;  
 therapy.

XX

OS Mus musculus.

XX

PN WO200053631-A1.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006182.

XX

PR 11-MAR-1999; 99US-00267901.

XX

PA (SCHE ) SCHERING CORP.

XX

PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;

XX

XX WPI; 2000-587426/55.

DR

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes, for  
PT polypeptides, and nucleic acids, useful in research, diagnosis and for  
PT treating inflammatory and autoimmune disorders.  
XX  
PS  
PS  
Claim 1; Page 21-22; 97pp; English.  
XX  
XX The present sequence is that of mouse cytokine-like factor-1 (CLF-1), a  
CC cytokine receptor family protein, which forms a complex with human  
CC interleukin-B60 (IL-B60, see AAB19586). The IL-B60/CLF-1 cytokine serves  
CC as a key physiological factor in motor neuron development and  
CC regeneration. A claimed soluble complex comprises at least 6 amino acids  
CC of mature IL-60B, at least 6 amino acids of mature CLF-1 or at least 6  
CC amino acids of mature CNTF-R. A claimed method of modulating the  
CC physiology or development of a cell or tissue culture cell involves  
CC contacting the cell with an agonist or antagonist of a complex comprising  
CC IL-60B and CLF-1 or CNTF-R. A claimed method of screening for a receptor  
CC which binds the complex involves contacting the complex with a cell  
CC expressing the receptor, to form a detectable interaction resulting in a  
CC physiological response in the cell  
XX  
SQ Sequence 407 AA;  
Query Match 95.4%; Score 2209.5; DB 3; Length 407;  
Best Local Similarity 99.8%; Pred. No. 1.7e-183;  
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 18 RPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77  
Db 1 RPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60  
QY 78 YWTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSLYVGLP 137  
Db 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSLYVGLP 119  
QY 138 PEKPFNISCWSRNKDLTCRWTPGAHTFHTNYSKYKLRWYGQDNTCEEYHTVGP 197  
Db 120 PEKPFNISCWSRNKDLTCRWTPGAHTFHTNYSKYKLRWYGQDNTCEEYHTVGP 179  
QY 198 CHIPKDALFPTPEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGLEDQLS 257  
Db 180 CHIPKDALFPTPEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGLEDQLS 239  
QY 258 VRWVSPALKDFLFOAKYQIRYRVSDVMKWVDDVSNQTSCLAGLKPCTVYFVQVRCN 317  
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDVMKWVDDVSNQTSCLAGLKPCTVYFVQVRCN 299  
QY 318 PFGIYGGKAGIWEWSHPTAASRTPSRPGCGGVCPEPRGGPSSGPRRRLKQFLGWL 377  
Db 300 PFGIYGGKAGIWEWSHPTAASRTPSRPGCGGVCPEPRGGPSSGPRRRLKQFLGWL 359  
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRGAARGPAG 425  
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRGAARGPAG 407  
RESULT 12  
AAB36648  
ID AAB36648 standard; protein; 407 AA.  
XX  
AC AAB36648;  
XX  
13-MAR-2001 (first entry)  
XX Mouse cytokine receptor subunit NR6 protein SEQ ID NO:5.  
DE  
XX  
KW DNAX cytokine receptor subunit; DCRS2; receptor protein;  
KW modulating cell proliferation; diagnosis; detection; drug screening;  
KW immunological disorder.  
XX  
OS Mus sp.  
XX  
FN WO200073451-A1.

XX 07-DEC-2000.  
PD  
XX 30-MAY-2000; 2000WO-US014867.  
PF  
XX  
XX 01-JUN-1999; 99US-00322913.  
PR  
XX (SCHE ) SCHERING CORP.  
PA  
XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;  
PI WPI; 2001-061536/07.  
XX  
XX Novel composition comprising DNAX cytokine receptor subunit polypeptide  
PT useful for regulating immune system function and for treating  
PT immunological disorders.  
XX  
XX Disclosure; Page 13-15; 93pp; English.  
XX  
XX The present invention describes a composition (I) comprising a  
CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The  
CC DCRS2 polypeptide is useful for binding ligands and for preparing cell  
CC antibodies. The DCRS2 polypeptide is also useful for modulating cell  
CC proliferation, for diagnostic and therapeutic applications, for detecting  
CC presence of their ligands and in drug screening assays. It is also useful  
CC for treating conditions such as immunological disorders. The present  
CC sequence represents a cytokine receptor subunit protein which is given in  
CC an alignment of various cytokine receptor subunits in the exemplification  
CC of the present invention  
XX  
SQ Sequence 407 AA;  
Query Match 95.4%; Score 2209.5; DB 4; Length 407;  
Best Local Similarity 99.8%; Pred. No. 1.7e-183;  
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 18 RPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77  
Db 1 RPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60  
QY 78 YWTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSLYVGLP 137  
Db 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSLYVGLP 119  
QY 138 PEKPFNISCWSRNKDLTCRWTPGAHTFHTNYSKYKLRWYGQDNTCEEYHTVGP 197  
Db 120 PEKPFNISCWSRNKDLTCRWTPGAHTFHTNYSKYKLRWYGQDNTCEEYHTVGP 179  
QY 198 CHIPKDALFPTPEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGLEDQLS 257  
Db 180 CHIPKDALFPTPEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGLEDQLS 239  
QY 258 VRWVSPALKDFLFOAKYQIRYRVSDVMKWVDDVSNQTSCLAGLKPCTVYFVQVRCN 317  
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDVMKWVDDVSNQTSCLAGLKPCTVYFVQVRCN 299  
QY 318 PFGIYGGKAGIWEWSHPTAASRTPSRPGCGGVCPEPRGGPSSGPRRRLKQFLGWL 377  
Db 300 PFGIYGGKAGIWEWSHPTAASRTPSRPGCGGVCPEPRGGPSSGPRRRLKQFLGWL 359  
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRGAARGPAG 425  
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRGAARGPAG 407  
RESULT 13  
ADC07180  
ID ADC07180 standard; protein; 407 AA.  
XX  
AC ADC07180;  
XX  
DT 18-DEC-2003 (first entry)  
XX

DE Mouse cytokine receptor subunit NR7.  
XX  
KW DNAX cytokine receptor subunit 2; DCRS2; cell physiology;  
KW cell development; cell culture; interferon detection;  
KW immune system disorder; NR6; mouse.  
XX  
OS Mus sp.  
XX  
FN US2003082734-A1.  
XX  
PD 01-MAY-2003.  
XX  
PF 18-SEP-2002; 2002US-00247463.  
XX  
PR 01-JUN-1999; 99US-0137159P.  
PR 31-MAY-2000; 2000US-00588113.  
XX  
PA (DOML/) DOWLING L M.  
PA (TIMA/) TIMANS J C.  
PA (GORM/) GORMAN D M.  
PA (KAST/) KASTELEIN R A.  
PA (BAZA/) BAZAN J F.  
XX  
XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;  
XX WPI; 2003-730048/69.  
XX  
DR Composition potentially useful for treating immunological disorders,  
PT comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a  
PT natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2  
PT sequence.  
XX  
XX Disclosure; SEQ ID NO 5; 41pp; English.  
XX  
PS The invention describes a composition of matter (I) comprising a  
XX substantially pure or recombinant DNAX cytokine receptor subunit 2  
CC (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein  
CC comprising a DCRS2 sequence. A composition of matter comprises: a  
CC substantially pure or recombinant DCRS2 polypeptide comprising at least  
CC three distinct nonoverlapping segments of at least four amino acids  
CC identical to segments of a fully defined 384 amino acid sequence (S1),  
CC given in the specification; a substantially pure or recombinant DCRS2  
CC polypeptide comprising at least two distinct nonoverlapping segments of  
CC at least five amino acids identical to segments of S1; a natural sequence  
CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.  
CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating  
CC physiology or development of a cell or cell culture. Antibodies to a  
CC DCRS2 can be used for quantitative detection of interferon. The DCRS2  
CC polypeptides and nucleic acids and their binding agents are potentially  
CC useful in treating and diagnosing disease, especially disease associated  
CC with the immune system. This is the amino acid sequence of mouse cytokine  
CC receptor subunit NR6 used in a comparison with DCRS2.  
XX  
XX Sequence 407 AA;  
SQ

Query Match 95.4%; Score 2209.5; DB 7; Length 407;  
Best Local Similarity 99.8%; Pred. No. 1.7e-183;  
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
18 RPLSLWSPLLLCVLGVPRGGSGAHTAVISPDPTLLIGSSLQATCSIHGDTFGATAEGL 77  
1 RPLSLWSPLLLCVLGVPRGGSGAHTAVISPDPTLLIGSSLQATCSIHGDTFGATAEGL 60  
78 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 137  
61 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 119  
138 PKPFPNISCWSNRKMDLTCRWTFPGARGETFLHTNYSKYLKRWYGDNTCEEYHTVGPHS 197  
120 PKPFPNISCWSNRKMDLTCRWTFPGARGETFLHTNYSKYLKRWYGDNTCEEYHTVGPHS 179  
198 CHIPKDLALFTPYEIVWEATNRLGARSVDLFLDVLVVVTPPPPHVSRVGGLEDQLS 257

Db 180 CHIPKDLALFTPYEIVWEATNRLGARSVDLFLDVLVVVTPPPPHVSRVGGLEDQLS 239  
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLRLAGLKEGTVYFVQVRN 317  
Db 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLRLAGLKEGTVYFVQVRN 299  
QY 318 PFGIYSGKAGIWSWSHPTAASTPRSERPPGPGGVCBPRGSPSSGPVRRRELKQFLGWL 377  
Db 300 PFGIYSGKAGIWSWSHPTAASTPRSERPPGPGGVCBPRGSPSSGPVRRRELKQFLGWL 359  
QY 378 KKHAYCSNLSPLRYDQWRAWMQKSHKTRNQDEGILPSSGRGAARGPAG 425  
Db 360 KKHAYCSNLSPLRYDQWRAWMQKSHKTRNQDEGILPSSGRGAARGPAG 407  
RESULT 14  
ADT90845  
ID ADT90845 standard; protein; 407 AA.  
XX  
AC ADT90845;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Mouse cytokine-like factor 1 (CLF-1).  
XX  
KW Interleukin; IL-B60; cytokine-like factor 1; CLF-1; CNTF-R;  
KW CNTF-receptor; inflammatory condition; autoimmune disorder; mouse.  
OS Mus sp.  
XX  
XX US2004192891-A1.  
XX  
PD 30-SEP-2004.  
XX  
PF 11-FEB-2004; 2004US-00778002.  
XX  
PR 11-MAR-1999; 99US-0124319P.  
PR 09-MAR-2000; 2000US-00521335.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;  
XX WPI; 2004-698788/68.  
DR GENBANK; NM\_004750.  
XX  
PT Novel mammalian cytokines, useful for producing antigen-antibody complex,  
PT treating conditions associated with abnormal physiology or development,  
XX including inflammatory conditions and/or autoimmune disorders.  
PS Claim 1; SEQ ID NO 13; 41pp; English.  
XX  
CC The invention relates to a complex comprising interleukin (IL)-B60,  
CC cytokine-like factor 1 (CLF-1) (partner sequence of IL-B60) and CNTF-R  
CC (CNTF-receptor). The complex is useful for producing an antigen-antibody  
CC complex, useful for treating conditions associated with abnormal  
CC physiology or development, including inflammatory conditions and/or  
CC autoimmune disorders and for generating antibodies which is useful in  
CC diagnostic applications. The present sequence is mouse cytokine-like  
CC factor 1 (CLF-1).  
XX  
SQ Sequence 407 AA;  
Query Match 95.4%; Score 2209.5; DB 8; Length 407;  
Best Local Similarity 99.8%; Pred. No. 1.7e-183;  
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
18 RPLSLWSPLLLCVLGVPRGGSGAHTAVISPDPTLLIGSSLQATCSIHGDTFGATAEGL 77  
1 RPLSLWSPLLLCVLGVPRGGSGAHTAVISPDPTLLIGSSLQATCSIHGDTFGATAEGL 60  
78 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 137

Db 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119  
QY 138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEYHTVGP 197  
Db 120 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEYHTVGP 179  
QY 198 CHIPKDLALFTPEYIWEATNRLGARSVDLTLVDVLTDDVTTDPDPVHVSRYGGLEDQLS 257  
Db 180 CHIPKDLALFTPEYIWEATNRLGARSVDLTLVDVLTDDVTTDPDPVHVSRYGGLEDQLS 239  
QY 258 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKGTVYFVQVRCN 317  
Db 240 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKGTVYFVQVRCN 299  
QY 318 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSGPRRRELKQFLGWL 377  
Db 300 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSGPRRRELKQFLGWL 359  
QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 425  
Db 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 407

## RESULT 15

ID ADT61033 standard; protein; 407 AA.

AC ADT61033;

XX 16-DEC-2004 (first entry)

XX Mouse cytokine-like factor 1 (CLF-1).

XX Cytokine; interleukin-B60; IL-B60; cell physiology; immune system;  
KW haematopoietic cell; immune disorder; T cell immune deficiency;  
KW chronic inflammation; tissue rejection; cardiovascular condition;  
KW neuropsychological condition; mouse; cytokine-like factor 1; CLF-1.

XX Mus sp.

XX US6800460-B1.

XX 05-OCT-2004.

XX 09-MAR-2000; 2000US-00521335.

XX 11-MAR-1999; 99US-0124319P.

XX (SCHE ) SCHERING CORP.

XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;

XX WPI; 2004-697202/68.

XX New isolated or non-human host cells transfected with expression vectors  
PT having nucleic acids encoding cytokines, useful in treating immune  
PT disorders, cardiovascular or neuropsychological conditions.

XX Disclosure; SEQ ID NO 13; 37pp; English.

XX The invention relates to mammalian interleukin-B60 (IL-B60). The  
CC invention also provides a method of producing a soluble complex  
CC comprising the mature protein portions of IL-B60 and CLF-1 polypeptides.  
CC The methods and compositions of the present invention are useful in  
CC controlling biology and physiology of mammalian cells, such as cells of a  
CC mammalian immune system, and in particular for regulating activation,  
CC development, differentiation and function of various cell types,  
CC including haematopoietic cells. They are specifically useful in treating  
CC abnormal medical conditions, including immune disorders, such as T cell  
CC immune deficiency, chronic inflammation or tissue rejection, or in  
CC cardiovascular or neuropsychological conditions. The present sequence is  
CC the mouse cytokine-like factor 1 (CLF-1).

SQ Sequence 407 AA;

Query Match 95.4%; Score 2209.5; DB 8; Length 407;  
Best Local Similarity 99.8%; Pred. No. 1.7e-183;  
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 18 RPLSLMSPFLILCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTTPGATAGL 77  
Db 1 RPLSLMSPFLILCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTTPGATAGL 60  
QY 78 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137  
Db 61 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119  
QY 138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEYHTVGP 197  
Db 120 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEYHTVGP 179  
QY 198 CHIPKDLALFTPEYIWEATNRLGARSVDLTLVDVLTDDVTTDPDPVHVSRYGGLEDQLS 257  
Db 180 CHIPKDLALFTPEYIWEATNRLGARSVDLTLVDVLTDDVTTDPDPVHVSRYGGLEDQLS 239  
QY 258 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKGTVYFVQVRCN 317  
Db 240 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKGTVYFVQVRCN 299  
QY 318 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSGPRRRELKQFLGWL 377  
Db 300 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSGPRRRELKQFLGWL 359  
QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 425  
Db 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 407

Search completed: April 11, 2006, 02:09:55

Job time : 117.124 secs

Result No.	Query	Score	Match	Length	DB	ID	Description
1	331	14.3	288	2	B59405	prolactin receptor	
2	331	14.3	376	2	A59405	prolactin receptor	
3	331	14.3	622	2	A40144	prolactin receptor	
4	339	14.2	918	2	A36337	membrane glycoprot	
5	319.5	13.8	917	2	I49699	glycoprotein 130 -	
6	317.5	13.7	918	2	I44629	interleukin-6 sign	
7	314	13.6	830	2	I50455	prolactin receptor	
8	312	13.5	310	2	A29884	prolactin receptor	
9	312	13.5	412	2	A41070	prolactin receptor	
10	312	13.5	610	2	A34631	lactogen receptor	
11	312	13.5	610	2	A36116	prolactin receptor	
12	307.5	13.3	292	2	I77525	prolactin receptor	
13	307.5	13.3	303	2	I77524	prolactin receptor	
14	307.5	13.3	608	2	I53269	prolactin receptor	
15	307.5	13.3	616	2	A30304	prolactin receptor	
16	306	13.2	831	2	JQ1655	prolactin receptor	
17	302.5	13.1	581	2	I45971	prolactin receptor	
18	261.5	11.3	630	2	I51086	prolactin receptor	
19	254.5	11.0	771	2	B38252	granulocyte colony	
20	254.5	11.0	783	2	JH0329	granulocyte colony	
21	254.5	11.0	863	2	C38252	granulocyte colony	
22	252.5	10.9	837	2	A34898	granulocyte colony	
23	234	10.1	372	2	I58141	ciliary neurotroph	
24	220.5	9.5	372	1	UHFUCN	ciliary neurotroph	
25	209.5	9.0	422	2	I37891	interleukin-11 rec	
26	208.5	9.0	432	2	I48343	interleukin-11 rec	
27	208	9.0	362	2	S60614	growth promoting a	
28	202.5	8.7	460	2	JL0145	interleukin-6 rece	
29	200.5	8.7	468	1	A41242	interleukin-6 rece	



Db	91	FTDIASLNTQLTCNLTITFGLEQNVYGITIIISGLPPEKPKNLSCVINEGKKRCRWDGGR	150
QY	163	HGETFLHTNYSKYKLRWYQDNTCEBYHTVGPSPHSCHPKDLALFTPYEIVWEATNRLGS	222
Db	151	--ETHLETNFTLKSEWATHKPADCAKADT--PTSCVDYSVTVFVNIWVWEAENALGK	206
QY	223	ARSDVLTLDVLVDVTTDPPDVHVSVRGLEQLSVRWVSPPALKDFLPQAKYQIRYRV	282
Db	207	VTSDHINFDPVVKVKNPNPNLNVINSELSLTKLTWN-PSIKSVII-LKYNIOYRTK	264
QY	283	DSVDWKV---DDVSNQTSCLAGLKPGTVYFVQVRCNPFPGIYGGKAGIWESEHPTAA	339
Db	265	DASTWSQIPEDTASTRSSFTVQDLKPFTYEVFRIR-----MKEDGKGYNSDWESEASG	319
QY	340	STPRSERP	347
Db	320	IT-YEDRP	326
RESULT 5			
I49699			
Glycoprotein 130 - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004			
C:Accession: I49699; I48370			
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.			
J. Immunol. 148, 4066-4071, 1992			
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130			
A:Reference number: I48370; MUID:192291532; PMID:1602143			
A:Accession: I49699			
A>Status: translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-917 <RES>			
A:Cross-references: UNIPROT:Q00560; UNIPARC:UPI000002845A; GB:M83336; NID:gl93591; PIDN:			
A:Accession: I48370			
A>Status: translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-917 <RE2>			
A:Cross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PI			
C:Genetics:			
A:Gene: gp130			
C:Keywords: Glycoprotein			
F:134-314/Domain: cytokine receptor homology <CRS>			
Query Match 13.8%; Score 319.5; DB 2; Length 917;			
Best Local Similarity 29.6%; Pred. No. 1.2e-16;			
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;			
QY	46	ISPDQPTLLIGSSLOATCSIHG---DTPGATAEGLYWTINGRRRLPSELRLNTSTLALA	102
Db	31	IYPEFPVQVQSGNFTATCVLKEACIQHYVYVNAIYVWKTNHAAPREQVTVINRTTSVT	90
QY	103	LANLNGSRQQSDNLVCHARDGSIILAGSLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA	162
Db	91	FTDVLVPSVQLTCNLSIFQIEQNVYVVTMLSGFPDPKPTNLTCTVINEGKNMLCQWDPCR	150
QY	163	HGETFLHTNYSKYKLRWYQD-NTCEEYHTVGPSPHSCHPKDLALFTPYEIVWEATNRLG	221
Db	151	--ETYLETNYTLKSE--WATERKPPDCQKHGT---SCMVSVMPTYYVNIWVWEAENALG	203
QY	222	SARSDVLTLDVLVDVTTDPPDVHVSVRGLEQLSVRWVSPPALKDFLPQAKYQIRYRV	281
Db	204	KVSSSEINFPDVKVKPFPNMLSVTNSELSLKLWVSSGL--GGLLDKSDIQYRT	261
QY	282	EDSDVWKV---DDVSNQTSCLAGLKPGTVYFVQVRCNPFPGIYGGKAGIWESEHPTA	338
Db	262	KDASTWIOVPLEDTWSPTSFVQDLKPFTYEVFRIR-----SIKDSGK-GYNSDWESEAS	316
QY	339	AST--PRSERP	347
Db	317	GTTYEDRPSRP	327

RESULT 6			
A44257			
interleukin-6 signal transducing molecule gp130 - rat			
C:Species: Rattus norvegicus (Norway rat)			
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004			
C:Accession: A44257			
R:Wang, Y.; Neibitt, J.E.; Fuentes, N.L.; Fuller, G.M.			
Genomics 14, 666-672, 1992			
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin			
A:Reference number: A44257; MUID:93052397; PMID:1427893			
A:Accession: A44257			
A>Status: preliminary; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-918 <WAN>			
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8			
A:Experimental source: liver			
A>Note: sequence extracted from NCBI backbone (NCBIP:118488)			
C:Keywords: transmembrane protein			
F:134-315/Domain: cytokine receptor homology <CRS>			
Query Match 13.7%; Score 317.5; DB 2; Length 918;			
Best Local Similarity 29.8%; Pred. No. 1.8e-16;			
Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;			
QY	46	ISPDQPTLLIGSSLOATCSIHG---DTPGATAEGLYWTINGRRRLPSELRLNTSTLALA	102
Db	31	IYPEFPVQVQSGNFTATCVLKEKCLQVYVNAIYVWKTNHAAPREQVTVINRTASSVT	90
QY	103	LANLNGSRQQSDNLVCHARDGSIILAGSLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA	162
Db	91	FTDVLVQNVQLTCNLSIFQIEQNVYVVTMLSGFPDPKPTNLTCTVINEGKNMLCQDLPCR	150
QY	163	HGETFLHTNYSKYKLRWYQD-NTCEEYHTVGPSPHSCHPKDLALFTPYEIVWEATNRLG	221
Db	151	--ETYLETNYTLKSE--WATERKPPDCRKYH--GTSSCMWGYTPYFVNIWVWEAENALG	204
QY	222	SARSDVLTLDVLVDVTTDPPDVHVSVRGLEQLSVRWVSPPALKDFLPQAKYQIRYRV	281
Db	205	NVSSSEINFPDVKVKPFPNMLSVTNSELSLKLWVNSGL--DSLRLKSDIQYRT	262
QY	282	EDSDVWKV---DDVSNQTSCLAGLKPGTVYFVQVRCNPFPGIYGGKAGIWESEHPTA	338
Db	263	KDASTWIOVPLEDTVSPRTSFVQDLKPFTYEVFRIR---SIKENGK-GYNSDWE-BA	316
QY	339	ASTPRSERP	347
Db	317	GTTYEDRDP	325
RESULT 7			
I50455			
prolactin receptor - pigeon			
C:Species: Columba livia (domestic pigeon)			
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004			
C:Accession: I50455			
R:Chen, X.; Horseman, N.D.			
Endocrinology 135, 269-276, 1994			
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.			
A:Reference number: I50455; MUID:94283267; PMID:7516866			
A:Accession: I50455			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-830 <CRB>			
A:Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:g466381; PI			
F:36-220/Domain: cytokine receptor homology <CRS1>			
F:240-426/Domain: cytokine receptor homology <CRS2>			
Query Match 13.6%; Score 314; DB 2; Length 830;			
Best Local Similarity 37.1%; Pred. No. 2.9e-16;			
Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;			
QY	137	PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH--TNSLYKLRWYQDNTCEEYHTVGP	195



C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: A36116  
R:Shirotta, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, J.  
Mol. Endocrinol. 4, 1136-1143, 1990  
A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.  
A:Reference number: A36116; MUID:91155946; PMID:2293022  
A:Accession: A36116  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-610 <SHI>  
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170ADB; GB:M57668; NID:g206366; PIDN:  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 312; DB 2; Length 610;  
Best Local Similarity 35.4%; Pred. No. 2.8e-16;  
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLYGLPPEKPFNISCWNRNMKDLTCRWPGAHGETFLHTNYSKYKLRWYQD 184  
DB 15 SLKQGS-----PPGKPEIHKCRSPDKETFTCWNFGTDGG--LPTNYSLTYSKE--GSK 65

QY 185 NT--CEYHTVPGHSCHPKD-LALFTPEIWEATNRLGARSVDLTLDVLDVTTDPP 241  
DB 66 TTYECPDYKTSFNSCFKQYTSIWKIYIITVNATNMGSSSDPLYVDVTIIVEPEPP 125

QY 242 PDVHVSRLGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDSDVKWVDDVSNQ 296  
DB 126 RNLT-L-EVKQLDKKTYLWVKSPPITDVKTGWFTMEYIRLKEAEWE--IHFTGHQ 183

QY 297 TSCRLAGLPGTVYFVQVRCNPGIYSGKAGIWSWSHPTAASP 342  
DB 184 TQKVPFDLYPGQKYLVTQCKP-----DHGYWSRWSSQESSVEMP 222

RESULT 12  
177525  
prolactin receptor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I77525  
R:Davis, J.A.; Linzer, D.I.H.  
Mol. Endocrinol. 3, 674-680, 1989  
A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
A:Reference number: I57699; MUID:89261824; PMID:2725531  
A:Accession: I77525  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-292 <CRS>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B198; GB:M22959; NID:g200481; PIDN:  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.3%; Score 307.5; DB 2; Length 292;  
Best Local Similarity 32.6%; Pred. No. 2.5e-16;  
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

QY 90 LSRLLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPFNISCWSR 149  
DB 1 MSSALAYMLLVLSISLNG--QS-----PPGKPEIHKCRSP 34

QY 150 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNT--CEYHTVPGHSCHPKD-LAL 206  
DB 35 DKETFTCWNPGSDGG--LPTNYSLTYSKE--GKNTYECPDYKTSFNSCFKQYTSI 90

QY 207 FTFPEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRLGLEDQLSVRWVS--PP 264  
DB 91 WKIYIITVNATNMGSSSDPLYVDVTIIVEPEPPRNLT-L-EVKQLDKKTYLWVKWLP 149

RESULT 13  
177524  
prolactin receptor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I77524  
R:Davis, J.A.; Linzer, D.I.H.  
Mol. Endocrinol. 3, 674-680, 1989  
A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
A:Reference number: I57699; MUID:89261824; PMID:2725531  
A:Accession: I77524  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-303 <CRS>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B197; GB:M22958; NID:g200479; PIDN:  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.3%; Score 307.5; DB 2; Length 303;  
Best Local Similarity 32.6%; Pred. No. 2.6e-16;  
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

QY 90 LSRLLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPFNISCWSR 149  
DB 1 MSSALAYMLLVLSISLNG--QS-----PPGKPEIHKCRSP 34

QY 150 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNT--CEYHTVPGHSCHPKD-LAL 206  
DB 35 DKETFTCWNPGSDGG--LPTNYSLTYSKE--GKNTYECPDYKTSFNSCFKQYTSI 90

QY 207 FTFPEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRLGLEDQLSVRWVS--PP 264  
DB 91 WKIYIITVNATNMGSSSDPLYVDVTIIVEPEPPRNLT-L-EVKQLDKKTYLWVKWLP 149

RESULT 14  
153269  
prolactin receptor, long form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I53269; JT0671; S34356  
R:Clarke, D.L.; Linzer, D.I.H.  
Endocrinology 133, 224-232, 1993  
A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.  
A:Reference number: I53269; MUID:93307149; PMID:8319571  
A:Accession: I53269  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-608 <CRS>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020890; GB:L14811; NID:g293769; PIDN:  
R:Moore, R.C.; Oka, T.  
Gene 134, 263-265, 1993  
A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form  
A:Reference number: JT0671; MUID:94085788; PMID:8262385  
A:Accession: JT0671  
A:Molecule type: mRNA  
A:Residues: 1-608 <MOO>  
A:Cross-references: UNIPARC:UPI0000020890; GB:L13593; NID:g347398; PIDN:AAC37641.1; PID  
R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.  
submitted to the EMBL Data Library, June 1993  
A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.  
A:Reference number: S34356

A;Accession: S34356  
A:Molecule type: mRNA  
A;Residues: 1-557,'P',559-608 <EDE>  
A;Cross-references: UNIPARC:UPI0000163B24; EMBL:G312696; PIDN:CAA51789.1; P1  
C;Comment: Prolactin receptor have long form and short form which are resulted from alte  
C;Comment: This long form receptor is capable of transducing a signal to milk protein ge  
C;Keywords: receptor; transmembrane protein  
F;31-216/Domain: cytokine receptor homology <CRS>  
F;230-253/Domain: transmembrane #status predicted <TMM>

Query Match 13.3%; Score 307.5; DB 2; Length 608;  
Best Local Similarity 32.6%; Pred.No. 6.2e-16;  
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

Qy 90 LSRLLNTSTIALALANLNGSRQSGDNLVCHARDGSILAGSCLYVLGPPEKPFNISCMWSR 149  
Db 1 MSSALAYMLLVLSISLNG--QS-----PPGKEIHKCRSP 34

Qy 150 NMKDLCRWTPPGAHGETFLHTNYSLKYKLRYWGQDNVT--CEEYHVTGPHSCHIPKD-LAL 206  
Db 35 DKETFTCWNPFGSDGG--LPTNYSLAYSYSE--GEKTYECPDYKTSGPNSCFFSKQYTISI 90

Qy 207 FTYEIVWEATNRLGSARSDLTLVDLVVVTTDPDPDVHSRVGGLEDQLSVRWYS--PP 264  
Db 91 WKYIIITVNATNEMGSTSDPLVDVTYIVEPEPRNLTL-EVKQLKDKKKTLWVKWLPP 149

Qy 265 ALKDF---LFQAQYQIRYRVEDSVDMKVDDVSNOTSCRLAGLKPGTVVFVQVRGNPFGI 321  
Db 150 TIIDVTKGTWTMYEIRLKSDEADEWE-IHFTGHQTQPKVFDLYPOQKYLVTQRCKP--- 205

Qy 322 YGSKKAGIWSEWHPTAASTP 342  
Db 206 ----DHGYWSRWGQEKSIPI 222

RESULT 15  
A30304  
prolactin receptor 2 precursor - rabbit  
N;Alternate names: prolactin receptor, mammary gland  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: A30304; A60380  
R;Entry: M.; Jolicœur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin,  
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989  
A;Title: Identification and sequence analysis of a second form of prolactin receptor by  
A;Reference number: A30304; MUID:89184578; PMID:2928321  
A;Accession: A30304  
A:Molecule type: mRNA  
A;Residues: 1-616 <EDE>  
A;Cross-references: UNIPROT:P14787; UNIPARC:UPI0000132237; GB:J04510; NID:g165669; PIDN:  
R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
Int. J. Biochem. 22, 1089-1095, 1990  
A;Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto  
A;Reference number: A60380; MUID:91146782; PMID:2289615  
A;Accession: A60380  
A:Molecule type: protein  
A;Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105-'NX',108,150-164,'XX',167  
A;Cross-references: UNIPARC:UPI000017C5D9; UNIPARC:UPI000017C5DA; UNIPARC:UPI000017C5DB;  
A;Note: the amino end of the mature protein was blocked  
C;Keywords: blocked amino end; glycoprotein; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-616/Product: prolactin receptor 2 #status predicted <MAT>  
F;36-221/Domain: cytokine receptor homology <CRS>  
F;235-258/Domain: transmembrane #status predicted <TMM>  
F;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.3%; Score 307.5; DB 2; Length 616;  
Best Local Similarity 36.3%; Pred.No. 6.3e-16;  
Matches 77; Conservative 28; Mismatches 90; Indels 17; Gaps 7;

Qy 137 PPEKPFNISCRMNKDLTCRWTPGAHGTEFLHTNYSCLKLRWYGQDNVTCEEYHVTGVPH 196  
Db 27 PEGKPFYFKCSRPSKETFTFCWRFGADGG--LPNTYLTLYHKEGTTTHCEPDYKTGGPN 84

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: April 11, 2006, 02:04:23 ; Search time 126.589 Seconds  
 (without alignments)  
 2368.694 Million cell updates/sec  
 Title: US-09-037-657-15  
 Perfect score: 2317  
 Sequence: 1 MPAGRPGVPAQSARPPRL.....NQDEGLPSRRGAARGPAG 425  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
 Total number of hits satisfying chosen parameters: 2166443  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_05.80.\*  
 1: uniprot\_sprot.\*  
 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2317	100.0	425	1	CRLF1_MOUSE
2	2176.5	93.9	422	1	CRLF1_HUMAN
3	1414.5	61.0	389	2	O6DG28_BRARE
4	1378.5	59.5	394	2	O6UAQ5_TETNG
5	995	42.9	437	2	O4RMP5_TETNG
6	468.5	20.2	207	2	O4TCM7_TETNG
7	416	18.0	151	2	O4RDR1_TETNG
8	380	16.4	199	2	O4RDQ9_TETNG
9	371	16.0	918	2	O9W6U9_CHICK
10	355.5	15.3	881	2	O57519_XENLA
11	332	14.3	268	2	O8TD78_HUMAN
12	331	14.3	288	2	O9GP36_HUMAN
13	331	14.3	349	2	O9UHJ5_HUMAN
14	331	14.3	376	2	O9GP35_HUMAN
15	331	14.3	622	1	PRLR_HUMAN
16	331	14.3	622	2	Q5RAM0_PONPY
17	330.5	14.3	1010	2	Q7TQ89_RAT
18	329	14.2	857	2	Q5FC04_HUMAN
19	329	14.2	918	1	IL6RB_HUMAN
20	319.5	13.8	917	1	IL6RB_MOUSE
21	319.5	13.8	917	2	O6PDI9_MOUSE
22	317.5	13.7	918	1	IL6RB_RAT
23	316	13.6	622	2	Q9N0J7_CALJA
24	314.5	13.6	608	2	Q99JZ1_MOUSE
25	314	13.6	622	2	O865V4_CEBAP
26	314	13.6	830	1	PRLR_COLLI
27	312	13.5	310	2	Q58DZ7_RAT
28	312	13.5	610	1	PRLR_RAT
29	307.5	13.3	292	2	O8C7G1_MOUSE
30	307.5	13.3	608	1	PRLR_MOUSE
31	307.5	13.3	616	1	PRLR_RABIT

32	307	13.2	625	1	PRLR_PIG	O6Jta8 sus scrofa
33	306	13.2	460	2	Q7T2Z0_CHICK	Q7T2Z0 gallus gall
34	306	13.2	581	1	PRLR_SHEEP	O46561 ovis aries
35	306	13.2	831	1	PRLR_CHICK	O04594 gallus gall
36	306	13.2	831	2	Q6QDA0_CHICK	Q6QDA0 gallus gall
37	305	13.2	831	1	PRLR_MELGA	Q91094 meleagris g
38	303	13.1	581	1	PRLR_CEREL	Q28235 cervus elap
39	302.5	13.1	581	1	PRLR_BOVIN	Q28172 bos taurus
40	294	12.7	611	2	O9PTH9_XENLA	O9pth9 xenopus lae
41	289.5	12.5	604	2	O6UAP8_TETNG	O6uap8 tetraodon n
42	289	12.5	357	2	Q4SQD8_TETNG	Q4sqd8 tetraodon n
43	289	12.5	819	2	O616F7_EUBMA	O616f7 eublepharis
44	288.5	12.5	611	2	Q91BF6_XENLA	Q91bf6 xenopus lae
45	288.5	12.5	611	2	Q9PTI0_XENLA	Q9pti0 xenopus lae

## ALIGNMENTS

RESULT 1  
 CRLF1\_MOUSE  
 ID CRLF1\_MOUSE STANDARD; PRT; 425 AA.  
 AC Q9JMS8;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)  
 DE (CLF-1) (Cytokine receptor-like molecule 3) (CLM-3) (NR6).  
 GN Name=Crlf1; Synonyms=Crlm3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.  
 RP FUNCTION, AND TISSUE SPECIFICITY.  
 RX PubMed10359701; DOI=10.1016/S0960-9822(99)80266-8;  
 RA Alexander W.S., Rakar S., Robb L., Farley A., Willson T.A.,  
 Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,  
 Hasegawa M., Maeda M., Fabri L., Jachno K., Nash A., Metcalf D.,  
 Nicola N.A., Hilton D.J.;  
 RT "Suckling defect in mice lacking the soluble haemopoietin receptor  
 NR6.";  
 RL Curr. Biol. 9:605-608(1999).  
 [3]  
 PHOSPHORYLATION SITE SER-223.  
 RA Jin W.-H., Dai J., Zhou H., Xia Q.-C., Zou H.-P., Zeng R.;  
 RT "Phosphoproteomic analysis of mouse liver using immobilized metal  
 affinity purification and linear ion trap mass spectrometry.";  
 RL Rapid Commun. Mass Spectrom. 18:2169-2176(2004).  
 CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory  
 role in the immune system and during fetal development. May be  
 involved in nervous system development (by similarity). Plays an  
 essential role in the initiation and/or maintenance of suckling in  
 neonatal mice.  
 CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a  
 heteromeric complex with cardiotrophin-like cytokine (CLC); the  
 CRLP1/CLC complex is a ligand for the ciliary neurotrophic factor  
 receptor (CNTFR) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected  
 in the brain of adult mice.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 folding and thereby efficient intracellular transport and cell-  
 surface receptor binding.  
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3  
 subfamily.  
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
CC domain.  
CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----

CC EMBL; AB040038; BAA92777.1; -: mRNA.  
DR HSP; P40223; ICD9.  
DR Ensembl; ENSMUSG00000007888; Mus musculus.  
DR MGI; MGI:1340030; Crflf1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS00853; FN3; 2.  
DR PROSITE; PS00835; IG-LIKE; FALSE NEG.  
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;  
KW Repeat; Signal.  
FT SIGNAL 1 33 Potential.  
FT CHAIN 34 425 Cytokine receptor-like factor 1.  
FT DOMAIN 35 134 Ig-like C2-type.  
FT DOMAIN 137 232 Fibronectin type-III 1.  
FT DOMAIN 237 337 Fibronectin type-III 2.  
FT MOTIF 330 334 WSXWS motif.  
FT MOD\_RES 222 222 Phosphoserine.  
FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 107 107 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).  
FT DISULFID 146 156 By similarity.  
FT DISULFID 187 198 By similarity.  
FT SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;  
CC -----  
CC Best Local Similarity 100.0%; Score 2317; DB 1; Length 425;  
CC Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC -----  
QY 1 MPAGRPGVQAARRPRPLSSLSWPLLCVLGVRPGSGAHTAVISPDPTLLIGSSLQ 60  
Db 1 MPAGRPGVQAARRPRPLSSLSWPLLCVLGVRPGSGAHTAVISPDPTLLIGSSLQ 60  
QY 61 ATCSIHGDTPGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
Db 61 ATCSIHGDTPGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
QY 121 ARDGSILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW 180  
Db 121 ARDGSILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW 180  
QY 181 YGQDNTCEEYHTVGPCHIPKDLALFTPYEIVWEATNRLGSARSDVLIDLVDDVTTDP 240  
Db 181 YGQDNTCEEYHTVGPCHIPKDLALFTPYEIVWEATNRLGSARSDVLIDLVDDVTTDP 240  
QY 241 PPDVHVSRYVGGLEDQLSVRWSPALKDFLFQAKYQIRYRVDSVDKVVDDVSNQTSCK 300  
Db 241 PPDVHVSRYVGGLEDQLSVRWSPALKDFLFQAKYQIRYRVDSVDKVVDDVSNQTSCK 300  
QY 301 LAGLKEGTGVYVQVRCNPFGIYSGKAGIWESEHSPTAASRPRSGGGVCEPRGGE 360  
Db 301 LAGLKEGTGVYVQVRCNPFGIYSGKAGIWESEHSPTAASRPRSGGGVCEPRGGE 360  
QY 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSPFLYDQWRAWMQSHKTRNQDEGILPSGRGAA 420  
Db 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSPFLYDQWRAWMQSHKTRNQDEGILPSGRGAA 420  
QY 421 RGPAG 425

Db 421 RGPAG 425

CC RESULT 2  
CC CRFLF1 HUMAN  
ID CRFLF1 HUMAN STANDARD; PRT; 422 AA.  
AC Q75462; O9UHS;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)  
DE (CLF-1) (Zcytor5).  
GN Name=CRFLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE, SUBUNIT, SUBCELLULAR LOCATION, TISSUE  
RP SPECIFICITY, AND INDUCTION.  
RC TISSUE=Fetal lung;  
RX MEDLINE=98349389; PubMed=9686600;  
RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,  
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;  
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with  
RT members of the cytokine type I receptor family.";  
RL J. Immunol. 161:1371-1379(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Magrangeas F., Jacques Y., Minvielle S.;  
RT "Cloning and expression of a novel soluble protein containing  
RT hemopoietic cytokine receptor domains.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Lok S., Preenell S.R., Jellberg A.C., Gilbert T., Whitmore T.E.,  
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,  
RA Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzyzanski M.I., Skaleka U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [6]

RP PROTEIN SEQUENCE OF 38-52.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.; "Signal peptide prediction based on analysis of experimentally verified cleavage sites."; Protein Sci. 13:2819-2824 (2004).

RL [7]

RP INTERACTIONS WITH CLC AND CNTRF.  
RX MEDLINE=20423191; PubMed=1096616; DOI=10.1038/78765;  
RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H., Froger J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y., Gauchat J.-F., Gascan H.; "CLF associates with CLC to form a functional heteromeric ligand for the CNTRF receptor complex."; Nat. Neurosci. 3:967-972 (2000).

RL [8]

RP VARIANTS CISS HIS-81 AND ARG-374.  
RX MEDLINE=22428294; PubMed=12509788;  
RA Knappskog P.M., Majewski J., Livneh A., Nilsen P.T.E., Bringsli J.S., Ott J., Bonan H.; "Cold-induced sweating syndrome is caused by mutations in the CRLF1 gene."; Am. J. Hum. Genet. 72:375-383 (2003).

RL [9]

CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory role in the immune system and during fetal development. May be involved in nervous system development.

CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CNTRF).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Highest levels of expression observed in spleen, thymus, lymph node, appendix, bone marrow, stomach, in placenta, heart, thyroid and ovary. Strongly expressed also in fetal lung.

CC -!- INDUCTION: Up-regulated in fibroblast primary cell cultures under stimulation by IFN-gamma, TNF-alpha and IL-6.

CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

CC -!- DISEASE: Defects in CRLF1 are the cause of cold-induced sweating syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive disorder characterized by profuse sweating induced by cool surroundings (temperatures of 7 to 18 degrees Celsius). Additional abnormalities include a high-arched palate, nasal voice, depressed nasal bridge, inability to fully extend the elbows and kyphoscoliosis.

CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3 subfamily.

CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like) domain.

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DR EMBL; AF059293; AAC28335.1; -; mRNA.  
DR EMBL; AF073515; AAD39681.1; -; mRNA.  
DR EMBL; AF178684; AAD54385.1; -; mRNA.  
DR EMBL; AY358291; AAQ88658.1; -; mRNA.  
DR EMBL; BC044634; AAH44634.1; -; mRNA.  
DR HSSP; P40223; 1CD9.

DR Ensembl; ENSG00000006016; Homo sapiens.  
DR HGNC; HGNC:2364; CRLF1.  
DR MIM; 604237; -.  
DR MIM; 272430; -.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0019955; P:cytokine binding; IPI.  
DR GO; GO:0004872; P:receptor activity; TAS.  
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. .); TAS.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF000411; fn3; 2.  
DR PROSITE; PS50853; FN3; 2.  
DR PROSITE; PS50835; IG LIKE; FALSE NEG.  
KW Direct protein sequencing; Disease mutation; Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.  
KW SIGNAL 1 37 Cytokine receptor-like factor 1.  
FT CHAIN 38 422 Ig-like C2-type.  
FT DOMAIN 38 131 Fibronectin type-III 1.  
FT DOMAIN 134 229 Fibronectin type-III 2.  
FT MOTIF 234 334 WSXWS motif.  
FT MOD\_RES 327 331 Phosphoserine (By similarity).  
FT CARBOHYD 219 219 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 140 140 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 168 168 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 292 292 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 382 382 N-linked (GlcNAc. .) (Potential).  
FT DISULFID 143 153 By similarity.  
FT DISULFID 184 195 By similarity.  
FT VARIANT 81 81 R -> H (in CISS).  
FT VARIANT 374 374 L -> R (in CISS).  
FT CONFLICT 240 240 /FTID=VAR\_017865.  
FT CONFLICT 240 240 /FTID=VAR\_017866.  
SQ SEQUENCE 422 AA; 46302 MW; AD9DFCB01B84228 CRC64;  
Query Match 93.9%; Score 2176.5; DB 1; Length 422;  
Best Local Similarity 94.8%; Pred. No. 1.2e-163;  
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;  
QY 1 MPAGRPVQAQSARPPRPLSLWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSLQ 60  
Db 1 MPAGRRGPAQAQSARPP-PLLP-LLLVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57  
QY 61 ATCSIHGDTPGATAGLYWTLNGLRLPSELRLTLNLTSTLALANLNGSRQSGDNLVCH 120  
Db 58 ATCSVHGDPGATAGLYWTLNGLRLPSELRLTLNLTSTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW 180  
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW 177  
QY 181 YQDNTCEYHTVGPFSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDLVVTTDP 240  
Db 178 YQDNTCEYHTVGPFSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDLVVTTDP 237  
QY 241 PPDVHVSRVGGLEDQLSVRWVSPALKKDFLQAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
Db 238 PPDVHVSRVGGLEDQLSVRWVSPALKKDFLQAKYQIRYRVEDSVDMKVDDVSNQTSR 237  
QY 301 LAGLKPVTYFVQVRCNPFGIYSGKKAGIWSWSHPTAASPRSRPGGVCBPRGG 360  
Db 298 LAGLKPVTYFVQVRCNPFGIYSGKKAGIWSWSHPTAASPRSRPGGVCBPRGG 357  
QY 361 PSSGPRRELKQFLGWLKKHAYCSNLSFLYDQWRAMQSHKTRNQDREGILPSSRGAA 420  
Db 358 PSSGPRRELKQFLGWLKKHAYCSNLSFLYDQWRAMQSHKTRNQDREGILPSSRGAA 417  
QY 421 RQPA 424  
Db 418 RGPA 421

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RESULT 3
Q6DG28 BRARE PRELIMINARY; PRT; 389 AA.
ID Q6DG28 BRARE PRELIMINARY; PRT; 389 AA.
AC Q6DG28
DT 25-OCT-2004 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
Zgc:91992.
GN ORFNames=zgc:91992;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichman J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA and mouse cDNA sequences."
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
DR EMBL; BC076526; AAH76526.1; -; mRNA.
DR ZFIN; ZDB-GENE-040718-397; zgc:91992.
DR InterPro; IPR002996; CytKn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
KW Receptor; Repeat; Transmembrane.
SQ SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;

Query Match 61.0%; Score 1414.5; DB 2; Length 389;
Best Local Similarity 68.1%; Pred. No. 2.1e-103;
Matches 260; Conservative 48; Mismatches 67; Indels 7; Gaps 5;

QY 27 LLLCVLGVPRGGGAHTAVISPOPTLLIGSSIQATCSIHGDPGATAGLYWTLNGRL 86
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 LHLCAAGVL--SSSTQVATIPQDPALLIGSSLSLTATCSVNPFD-HGIHAGSLYWTLNGKRL 63
QY 87 PSELRLMTSTLTALANLNGSRQSGDNLVCHARDGSLAGSLCYVGLPPEKPNISC 146
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 PSSYSLISPTVISVTLPLRLSGRQRSGDNLVCHNGGHVLAGSLCYVGMPPKPNLTC 123
QY 147 WSNMMDLTCRWTPPGAHGETFLHTNYSKYLKRWYGQDNTCEYHTVGPHSCHIPKDAL 206
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 WSRNTKDLICRWAPGGQGETFIKTKYTLKRLWYGREKECEDYSTGEPTCYIPRDLAL 183

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QY 207 FTPYEIWEATNRLGARSVDLTLDVLTDPDPPDVHVSRLVGGLEDOLSVRWVSPRAL 266
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 FTPYEIWEASNLQGTATSDIYLDVLTDPDPPDVHVSRLVGGLEDOLTVRWGTPPAL 243
QY 267 KDFLFOAKYQIRYRVEDSDVMDVDDVSNQTSCLAGLKPGTVYFQVRCNPFYIGSKK 326
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 KDFLFOAKYQIRYRLSESDWKVDDVGNQTSCLAGLRPGTVYFQVRCNPFYIGLSRK 303
QY 327 AGINSEWSHPTAASRPSRPGGVCEPRGSGPSSGVRRELKQFLGWLKKHAY-CSN 385
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 AGISDWSHPTAASRPSRPGGVCEPRGSGPSSGVRRELKQFLGWLKKHAY-CSN 360
QY 386 LSFRLYDQRAWQKSHKTRNQ 407
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 MSIKLYDQRAWVWLQKSHKTRNQ 382

RESULT 4
Q6UAQ5 TETNG PRELIMINARY; PRT; 394 AA.
ID Q6UAQ5 TETNG PRELIMINARY; PRT; 394 AA.
AC Q6UAQ5;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Class I helical cytokine receptor number 1.
GN Name=CRPAL;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Maucell E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicad S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Binmont C., Skalli Z., Cattolico L., Poulain J., Berardinis Vd.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigs R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Crolius H.R.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL Nature 431:946-957(2004).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
DR EMBL; AY374473; AAR25664.1; -; mRNA.
DR Ensembl; AY374473; Tetraodon nigroviridis.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR002996; CytKn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00853; IG LIKE; 1.
KW Immunoglobulin domain; Receptor; Repeat; Transmembrane.
SQ SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;

Query Match 59.5%; Score 1378.5; DB 2; Length 394;
Best Local Similarity 67.6%; Pred. No. 1.5e-100;
Matches 259; Conservative 39; Mismatches 80; Indels 5; Gaps 4;

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QY 27 LLLCVLVPRG-GSGAHTAVISQDPTLLIGSSLOATCSIHGDTFGATAGLYWTNLGRR 85  
 DB 9 LLLLLHSPAVLALSTHVAIVYQDPVLRMGSNLTASCWIRSDI-GVHASSLFWTLNGQP 67  
 QY 86 LPSELRLNTSLALANLNGSQSGDNLVCHARDGSLAGSCLVGLPPEKPNIS 145  
 DB 68 LPSSLRVLSFTNLVSLAGLNARQTSQGNLVCHHHKHGLAGSCLVGVMPAKPVNLT 127  
 QY 146 CWSRNMKDLTCRWTPGAGHGTFLHTNYSKYKLRYGQDNTCEBYHTVGPHSCHIPKDLA 205  
 DB 128 CWSRNTKDLTCSWAPGGRGTHISTQYTLKYKLRYGKECEDYTHVQYSCSIITDLH 187  
 QY 206 LFTPEYIWIWATRLGSRARDVLTLDVLDVVTTPDPDVHVRVGGLEDQLSVRWVSPPA 265  
 DB 188 LFTPEYIWIWASQNGRATSDVITLDVLDVVTTPDPGSGVTVSRVQLEDQLSVRWEAPPA 247  
 QY 266 LKDFLOAKYQIIRVRVEDSDVWVDDVSNQTSRLAGLPGTVYFVQVRCNPPGLYGSK 325  
 DB 248 LKDFLOAKYQIIRYRLSDSDWKVMDVGNQTSRLAGLPGTVYFVQVRCNPPGLYGSR 307  
 QY 326 KAGIWESEWHSPTAASPRSRPGGVCPEPRGSPVRRRLKQFLGWLKXKHY-CS 384  
 DB 308 KAGIWESEWHSPTAASPHSERLMSGS--CDKSSADSNSLTRRLKQFLGWLKXKHYGCS 365  
 QY 385 NLSFRLYDQWRWQKSHKTRNQ 407  
 DB 366 SMSMKLYDQWRVLMQKSHKARNQ 388

## RESULT 5

Q4RMP5\_TETNG  
 ID Q4RMP5\_TETNG PRELIMINARY; PRT; 437 AA.  
 AC Q4RMP5;  
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
 DE Chromosome 10 SCAF15019, whole genome shotgun sequence.  
 DE (Fragment).  
 DE ORFNames=GSTENG00031935001;  
 GN Tetraodon nigroviridis (Green puffer).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Croliis H.;  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype."; Nature 431:946-957(2004).  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAB01015019; CAG10337.1; -; Genomic\_DNA.  
 FT NON TER 1  
 SQ SEQUENCE 437 AA; 49065 MW; 99F9602E88F95583 CRC64;

Query Match 42.9%; Score 995; DB 2; Length 437;  
 Best Local Similarity 53.8%; Pred. No. 3.9e-70;  
 Matches 199; Conservative 33; Mismatches 62; Indels 76; Gaps 5;  
 QY 44 AVISPODPTLLIGSSLOATCSIHGDTFGATAGLYWTNLGRRPSELRLNTSLAL 103  
 DB 1 AVIYQDPVLRMGSNLTASCWIRSDI-GVHASSLFWTLNGQPLPSSLYRVLSPTNLSVTL 59  
 QY 104 ANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPNIS 163  
 DB 60 AGLNARQTSQGNLVCHHHKHGLAGSCLVGVMPAKPVNLTCSWRNTKDLTCSWAPGR 119  
 QY 164 GETFLHTNYSKYKLRYGQDNTCEBYHTVGPHSCHIPKDLALFTPEYIWIWATRLGSA 223  
 DB 120 GETHISTQYTLKYKLRYGKECEDYTHVQYSCSIITDLHFTPEYIWIWASQNGRA 179  
 QY 224 RSDVLTLDVLDVVTTPDPDVHVRVGGLEDQLSVRWVSPPALKDFLOAKYQIRVRVED 283  
 DB 180 TSDVITLDVLDVVTTPDPGSGVTVSRVQLEDQLSVRWEAPPALKDFLOAKYQIRVRVED 239  
 QY 284 SVDWK-----VVDD 292  
 DB 240 SQDWKEKSAFDOERERANTEPLCILGLRVLMNEKYSVEAGPLQMALRLILLPVLWVDD 299  
 QY 293 VSNQTSRLAGLPGTVYFVQVRCNPPGLYGSKAG-----IWSWHSPTAASPRSRPG 348  
 DB 300 VGNQTSRLAGLPGTVYFVQV-----GPRSSASDRIMI-----SDRRV 339  
 QY 349 PGSGVCEPRG 358  
 DB 340 ASAGPLQPRG 349

## RESULT 6

Q4TCM7\_TETNG  
 ID Q4TCM7\_TETNG PRELIMINARY; PRT; 207 AA.  
 AC Q4TCM7;  
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF6801, whole genome shotgun sequence.  
 DE (Fragment).  
 DE ORFNames=GSTENG0003230001;  
 GN Tetraodon nigroviridis (Green puffer).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Croliis H.;  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype."; Nature 431:946-957(2004).  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

```

DR EMBL; CAEA01006801; CAF89355.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 22607 MW; 71F8E80B9998309F CRC64;

Query Match 20.2%; Score 468.5; DB 2; Length 207;
Best Local Similarity 48.3%; Pred. No. 6.9e-29;
Matches 102; Conservative 7; Mismatches 21; Indels 81; Gaps 4;

QY 231 DVLVDVVTDDPPDVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVDSVDWK-- 288
D 1 ECLPPTVTTDPPSGVTVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVDSVDWKKE 60
QY 289 -----VVDVNSQNTSC 299
D 61 KSAFDQERAWTEPLCILGLRLVMNEKYSVEAGPLQMALRLILLPVLVWMDVNGQNTSC 120
QY 300 RLAGLKPQTVY-----FVQVRCNPFGIYSGKKAGIWSWSHPT 337
D 121 RLAGLRPGTVYSRWDPGPVAPQOTGSGSLTAVSLPQVRCNPNVGIYSGRKAGIWSWSHPT 180
QY 338 AASTPRSERP----GFGGVGCEPRGGEPSG 364
D 181 AASTPHSGEPPLPAGPGRSL----GSAPESG 207

RESULT 7
Q4RDR1 TETNG
ID Q4RDR1 TETNG PRELIMINARY; PRT; 151 AA.
AC Q4RDR1
DT 13-SEP-2005 (TREMREL. 31, Created)
DT 13-SEP-2005 (TREMREL. 31, Last sequence update)
DT 13-SEP-2005 (TREMREL. 31, Last annotation update)
DE Chromosome undetermined SCAF15947, whole genome shotgun sequence.
GN ORFNames=GSTENG00037335001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAEA01015948; CAGL3473.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 199 AA; 21734 MW; 299786CDFB24BDEB CRC64;

Query Match 16.4%; Score 380; DB 2; Length 199;
Best Local Similarity 67.0%; Pred. No. 6.6e-22;
Matches 73; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 236 VTTDPPDPVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVDSVDWKVDDVSN 295
D 34 VTTDPPDPVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVDSVDWKVDDVSN 87
QY 296 QTSCLAGLKPQTVYFVQVRCNPFGIYSGKKAGIWSWSHPTAASTPRS 344
D 88 -----SVLWTVHFVQVRCNPNVGIYSGRKAGIWSWSHPTAASTPRS 128

RESULT 9
Q9W6U9_CHICK

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ID Q9W6U9\_CHICK PRELIMINARY; PRT; 918 AA.  
 AC Q9W6U9;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Glycoprotein 130 precursor.  
 GN Name=gpi30;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryonic heart primary culture;  
 RA MEDLINE=99026068; PubMed=9806927;  
 RX Geissen M., Heller S., Pennica D., Ernberger U., Rohrer H.;  
 RT "The specification of sympathetic neurotransmitter phenotype depends  
 on gpi30 cytokine receptor signaling.";  
 RL Development 125:4791-4801(1998).  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 folding and thereby efficient intracellular transport and cell-  
 surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 activation (By similarity).  
 DR EMBL; AJ011688; CAB42084.1; -; mRNA.  
 DR HSSP; P40189; 1BQJ.  
 DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hemtrecept\_1302.  
 DR InterPro; IPR010457; Lep\_receptor\_Ig.  
 DR Pfam; PF00041; fn3; 4.  
 DR Pfam; PF06328; Lep\_receptor\_Ig; 1.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS0853; FN3; 5.  
 DR PROSITE; PS0153; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
 DR Receptor; Repeat; Signal; Transmembrane.  
 KW SIGNAL  
 FT SIGNAL 1 26 Potential.  
 SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613BF CRC64;  
  
 Query Match 16.0%; Score 371; DB 2; Length 918;  
 Best Local Similarity 30.2%; Pred. No. 2.4e-20;  
 Matches 111; Conservative 41; Mismatches 138; Indels 78; Gaps 16;  
  
 QY 27 LLLCVLGVPRGGGAHTAVISQDPTLLIGSSIQATCSIHG---DTPGATAGLYWTLNG 83  
 Db 16 LNICFEV--SGGLVSCGHIIPESVPLAGSNFTALCIILNESCLDFGNIIYASQIIWKMN 74  
  
 QY 84 RRLPSELRLN-----TSTLALANLNGSRQSGDNLVCHA-RDGSI---LAG 129  
 Db 75 KVIPKEQYREINRTVSSVTFNFTSSLA-----SPLTCNVLDAGQIEQNIYG 120  
  
 QY 130 SCLYVGLPPEKPFNISC-----WSNMKDLTCRWTPGAGHGTFLHTNYSLKYLKRW 180  
 Db 121 ISVTVGLPPEKPNLSICVILSPKVEWYNN-----CTWNPGRH--TFLDTRFLKYMWR 173  
  
 QY 181 YQDNTCEHYHTVGHSCHPKDALFTPEYIIVWATNRLGARSQDVLTLVDLVVTTDP 240  
 Db 174 ETPFPCIPYVN---NSCTI--SDVOFFVNLEWVAANALGAESDHLVDFPIEIVKPP 229  
  
 QY 241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVSDSVWKVV---DVSNOT 297  
 Db 230 PRLNSVNS--GILPTVLKLSWEN--QISTVVMELKNIRYRISSDTNWMEVPEDTASPT 286  
  
 QY 298 SCRLAGLKPQTYVVOVRCNPFYIGSKKAGIWSWSHPTAASRPRSRPPGGGVCBPR 357  
 Db 287 SPSIQGLRPTYEYVFSIRC-----NKEDGVGFSDWSEIQIGVTTED----- 328  
  
 QY 358 GGEPSGGP 365  
 Db 329 --KPSKGP 334

RESULT 10  
 ID 057519\_XENLA PRELIMINARY; PRT; 881 AA.  
 AC 057519;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Gpi130p1.  
 GN Name=xgp130;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Chen J., Grace A., Chien K.R.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 folding and thereby efficient intracellular transport and cell-  
 surface receptor binding (By similarity).  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 activation (By similarity).  
 DR EMBL; AF041845; AAC03531.1; -; mRNA.  
 DR HSSP; P40189; 1BQJ.  
 DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003529; Hemtrecept\_1302.  
 DR InterPro; IPR010457; Lep\_receptor\_Ig.  
 DR Pfam; PF00041; fn3; 4.  
 DR Pfam; PF06328; Lep\_receptor\_Ig; 1.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS0853; FN3; 5.  
 DR PROSITE; PS0153; HEMATOPO\_REC\_L\_F2; UNKNOWN\_1.  
 DR Receptor; Repeat; Transmembrane.  
 KW SEQUENCE 881 AA; 99003 MW; 7DB7942D211138A0 CRC64;  
  
 Query Match 15.3%; Score 355.5; DB 2; Length 881;  
 Best Local Similarity 30.5%; Pred. No. 3.8e-19;  
 Matches 100; Conservative 43; Mismatches 136; Indels 49; Gaps 11;  
  
 QY 50 DPTLLIGS-SLOATCSIHGDTFGATAGLYWTLNGRRLPSELRLNTSTLALANLNG 108  
 Db 33 DPGIVHGERPPTAYCVINQTCRLREDASRIYLVKGVKVPETQYELINQTTSSVTFENLT 92  
  
 QY 109 SRQSGDNLVCHARGDSILAGSLYGLPPEKPFNISCWSNMKDLTCRWTPGAGHGTFL 168  
 Db 93 LNSPLTCNVMAAGSHVANTLYGIFFTGLPDPKPTNLTCTIVYNQDNLCTCTWDFGR--PTNL 150  
  
 QY 169 HTNYSLKYLKRW-----YQDNTCEHYHTVGHSCHPKDALFTPEYIIVWATNRL 220  
 Db 151 PNTYTLSH--RWAHFGANYCRGANNSC-----THSP-GFQFYIDTTQVEATNRL 198  
  
 QY 221 GSARSDVLTLVDLVVTTDPPDPVHVSRRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYR 280  
 Db 199 GIKQSETLTIDPNIVKPNPQPSLSSLELPNALKIEWKNPIT---NAFLKNYIRYR 255  
  
 QY 281 VEDSVQKVV---DVSNOTSCRLAGLKPQTYVVOVRCNPFYIGSKKAGIWSWSHPT 337  
 Db 256 PVKTDQWEMVPEDTASHRDSFTLQDLFPNTYEVYSIRC-----IHKDGHGFSDWSELK 310  
  
 QY 338 AASTPRSRPPGGGVCBPRGEGPSGGP 365  
 Db 311 KQVTP--EAP-----PSRGP 323  
  
 RESULT 11  
 Q8TD78\_HUMAN  
 ID Q8TD78\_HUMAN PRELIMINARY; PRT; 268 AA.  
 AC Q8TD78;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)





RA Gould D., Djiane J., Kelly P.A.;  
 RT "Identification of a cDNA encoding a long form of prolactin receptor  
 in human hepatoma and breast cancer cells";  
 RL Mol. Endocrinol. 3:1455-1461(1989).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RX MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;  
 RA Hu Z.-Z., Zhuang L., Meng J., Leonides M., Dufau M.L.;  
 RT "The human prolactin receptor gene structure and alternative promoter  
 utilization: the generic promoter hP111 and a novel human promoter  
 hp(N)";  
 RL J. Clin. Endocrinol. Metab. 84:1153-1156 (1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalón D.K., Murny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [5]  
 RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).  
 RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;  
 RA Fuh G., Wells J.A.;  
 RT "Prolactin receptor antagonists that inhibit the growth of breast  
 cancer cell lines";  
 RL J. Biol. Chem. 270:13133-13137 (1995).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.  
 RX MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;  
 RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;  
 RT "The X-ray structure of a growth hormone-prolactin receptor complex";  
 RL Nature 372:478-481 (1994).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 prolactin.  
 CC -!- INTERACTION:  
 CC P51956:NEK3; NbExp=1; IntAct=EBI-476182, EBI-476041;  
 CC P52735:VAV2; NbExp=1; IntAct=EBI-476182, EBI-297549;  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=P16471-1; Sequence=Displayed;  
 CC Name=2; Synonyms=delta-S1;  
 CC IsoId=P16471-2; Sequence=VSP\_001720;  
 CC Name=3;  
 CC IsoId=P16471-3; Sequence=VSP\_012620, VSP\_012621;  
 CC Note=Soluble isoform that appears specific for the ET-474 breast

CC cancer cell line;  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding.  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation.  
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; M31661; AAA60174.1; -; mRNA.  
 DR EMBL; AF091870; AAD32032.1; -; Genomic DNA.  
 DR EMBL; AF091863; AAD32032.1; JOINED; Genomic DNA.  
 DR EMBL; AF091864; AAD32032.1; JOINED; Genomic DNA.  
 DR EMBL; AF091865; AAD32032.1; JOINED; Genomic DNA.  
 DR EMBL; AF091867; AAD32032.1; JOINED; Genomic DNA.  
 DR EMBL; AF091868; AAD32032.1; JOINED; Genomic DNA.  
 DR EMBL; AF091869; AAD32032.1; JOINED; Genomic DNA.  
 DR EMBL; AF349939; AAK32703.1; -; mRNA.  
 DR EMBL; BC059392; AAH59392.1; -; mRNA.  
 DR EMBL; S78505; AAB34470.1; -; mRNA.  
 DR PIR; A40144; A40144.  
 DR PDB; 1BP3; X-ray; B=25-235.  
 DR IntAct; P16471; -;  
 DR ENSEMBL; ENSG00000113494; Homo sapiens.  
 DR HGNC; HGNC:9446; PRLR.  
 DR MIM; 176761; -;  
 DR GO; GO:0009986; C:cell surface; IDA.  
 DR GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.  
 DR GO; GO:0004803; F:prolactin receptor activity; NAS.  
 DR GO; GO:0004923; F:protein homodimerization activity; NAS.  
 DR GO; GO:0006916; P:anti-apoptosis; NAS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NAS.  
 DR GO; GO:0007566; P:embryo implantation; TAS.  
 DR GO; GO:0007595; P:lactation; NAS.  
 DR GO; GO:0006694; P:steroid biosynthesis; NAS.  
 DR GO; GO:0042110; P:T cell activation; NAS.  
 DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.  
 DR GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.  
 DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
 DR InterPro; IPR003961; FN\_III  
 DR InterPro; IPR003528; HemtreceptL\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR PROSITE; PS00853; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO REC L F1; 1.  
 DR 3D-structure; Alternative splicing; Glycoprotein; Receptor; Repeat;  
 KW Signal; Transmembrane.  
 KW SIGNAL 1 24  
 FT CHAIN 25 622 Prolactin receptor.  
 FT TOPO\_DOM 25 234 Extracellular (Potential).  
 FT TRANSMEM 235 258 Potential.  
 FT TOPO\_DOM 259 622 Cytoplasmic (Potential).  
 FT DOMAIN 27 121 Fibronectin type-III 1.  
 FT DOMAIN 127 227 Fibronectin type-III 2.  
 FT MOTIF 215 219 WSXWS motif.  
 FT MOTIF 267 275 Box 1 motif.  
 FT CARBOHYD 59 59 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 233 233 N-linked (GlcNAc. .) (Potential).  
 FT DISULFID 36 46 By similarity.  
 FT DISULFID 75 86 By similarity.  
 FT VARSPPLIC 24 124 Missing (in isoform 2).  
 FT VARSPPLIC 229 230 /FTId=VSP\_001720.  
 FT VARSPPLIC 231 622 DF -> AW (in isoform 3).  
 FT VARSPPLIC /FTId=VSP\_012620.  
 FT Missing (in isoform 3).



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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:16:39 ; Search time 29.3685 Seconds  
(without alignments)  
1196.422 Million cell updates/sec

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Perfect score: 2317  
Sequence: 1 MPAGRPVQSGARRPRRL.....NODEGILPSGRGAARGPAG 425

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/PCTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2288	98.7	425	2	US-09-071-224-6
2	2209.5	95.4	407	2	US-09-521-335-13
3	2209	95.3	405	2	US-09-012-072-2
4	2209	95.3	405	2	US-09-120-601-2
5	2176.5	93.9	422	2	US-09-866-028-32
6	2176.5	93.9	422	2	US-09-944-457-32
7	2176.5	93.9	422	2	US-09-945-584-32
8	2176.5	93.9	422	2	US-09-944-944-32
9	2176.5	93.9	422	2	US-09-945-587-32
10	2172.5	93.8	422	2	US-09-071-224-2
11	2097	90.5	385	2	US-09-071-224-19
12	2095	90.4	410	2	US-09-521-335-12
13	2094	90.4	425	2	US-09-071-224-4
14	2071.5	89.4	448	2	US-09-120-601-6
15	2051	88.5	388	2	US-09-071-224-17
16	2035	87.8	385	2	US-09-071-224-20
17	2011.5	86.8	434	2	US-09-012-072-4
18	2011.5	86.8	434	2	US-09-120-601-4
19	1978	85.4	392	2	US-09-071-224-18
20	1963	84.7	389	2	US-09-071-224-28
21	1962	84.7	389	2	US-09-071-224-22
22	1961	84.6	389	2	US-09-071-224-29
23	1960	84.6	389	2	US-09-071-224-30
24	1959	84.5	389	2	US-09-071-224-24
25	1959	84.5	389	2	US-09-071-224-25
26	1959	84.5	389	2	US-09-071-224-27
27	1958	84.5	389	2	US-09-071-224-26

28	1957	84.5	389	2	US-09-071-224-31
29	1602	69.1	303	2	US-09-071-224-23
30	1598	69.0	303	2	US-09-071-224-21
31	334	14.4	1168	2	US-09-313-942-24
32	334	14.4	1168	2	US-10-282-162-24
33	331	14.3	332	2	US-09-313-942-10
34	331	14.3	332	2	US-10-282-162-10
35	331	14.3	349	2	US-08-806-597A-14
36	331	14.3	349	2	US-08-970-428A-14
37	331	14.3	637	2	US-09-949-016-10128
38	331	14.3	1158	2	US-09-313-942-26
39	331	14.3	1158	2	US-10-282-162-26
40	329	14.2	488	1	US-08-599-455B-5
41	329	14.2	488	2	US-09-069-781B-5
42	329	14.2	488	2	US-09-137-132-5
43	329	14.2	488	2	US-08-864-564A-5
44	329	14.2	488	2	US-09-094-410-5
45	329	14.2	488	2	US-08-708-123D-5

ALIGNMENTS

RESULT 1  
US-09-071-224-6  
; Sequence 6, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Jelbert, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-071-224-6

Query Match 98.7%; Score 2288; DB 2; Length 425;  
Best Local Similarity 98.8%; Pred. No. 2.3e-205;  
Matches 420; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAGRGVVAQSAARPPRLSLWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSIQ 60  
DB 1 MPAGGGAQSAARPPRLSLWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSIH 60

QY 61 ATCSIHGDTFGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120  
DB 61 ATCSIHGDTFGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPPKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
DB 121 ARDGSILAGSCLYVGLPPPKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEBYHTVGPHSCHI PKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240  
DB 181 YQDNTCEBYHTVGPHSCHI PKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240

QY 241 PPDVHVSRYGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSR 300  
DB 241 PPDVHVSRYGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSR 300

QY 301 LAGLKPGETVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSERPGGGVCEPRGGE 360  
DB 301 LAGLKPGETVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSERPGGGVCEPRGGE 360

QY 361 PSSGPVRRBKQFLGWLKHHAYCSNLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRGAA 420  
DB 361 PSSGPVRRBKQFLGWLKHHAYCSNLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRGAA 420

QY 421 RGPAG 425  
DB 421 RGPAG 425

RESULT 2  
US-09-521-335-13  
; Sequence 13, Application US/09521335  
; Patent No. 6800460  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/09/521,335  
; CURRENT FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 407  
; TYPE: PRT  
; ORGANISM: rodent  
US-09-521-335-13

Query Match 95.4%; Score 2209.5; DB 2; Length 407;  
Best Local Similarity 99.8%; Pred. No. 4.6e-198;  
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 18 RPLSSLSWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGL 77  
DB 1 RPLSSLSWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGL 60

QY 78 YWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 137  
DB 61 YWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 119

QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHS 197

DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHS 179

QY 198 CHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLS 257  
DB 180 CHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLS 239

QY 258 VRWVSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSRLAGLKPGETVYFVQVRCN 317  
DB 240 VRWVSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSRLAGLKPGETVYFVQVRCN 299

QY 318 PFIYGSKKAGIWSWSHPTAASPRSERPGGGVCEPRGGEPSGPRRELKQFLGWL 377  
DB 300 PFIYGSKKAGIWSWSHPTAASPRSERPGGGVCEPRGGEPSGPRRELKQFLGWL 359

QY 378 KKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRGGAARGPAG 425  
DB 360 KKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRGGAARGPAG 407

RESULT 3  
US-09-012-072-2  
; Sequence 2, Application US/09012072  
; Patent No. 6060276  
; GENERAL INFORMATION:  
; APPLICANT: Masiakowski, Piotr  
; TITLE OF INVENTION: No. 6060276el Orphan Receptors  
; FILE REFERENCE: REG 630  
; CURRENT APPLICATION NUMBER: US/09/012,072  
; CURRENT FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: MOUSE  
US-09-012-072-2

Query Match 95.3%; Score 2209; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 5.1e-198;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SSLWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGLYWT 80  
DB 1 SSLWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGLYWT 60

QY 81 LNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLPPEK 140  
DB 61 LNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLPPEK 120

QY 141 PFNISCWSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHSCHI 200  
DB 121 PFNISCWSWRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHSCHI 180

QY 201 PKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLSVRW 260  
DB 181 PKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPPDVHVSRYGGLEDQLSVRW 240

QY 261 VSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSRLAGLKPGETVYFVQVRCNPF 320  
DB 241 VSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSRLAGLKPGETVYFVQVRCNPF 300

QY 321 IYGSKKAGIWSWSHPTAASPRSERPGGGVCEPRGGEPSGPRRELKQFLGWLKXH 380  
DB 301 IYGSKKAGIWSWSHPTAASPRSERPGGGVCEPRGGEPSGPRRELKQFLGWLKXH 360

QY 381 AYCNSLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRGGAARGPAG 425  
DB 361 AYCNSLSFRLYDQWRAWMOKSHKTRNQDEGILPSGRGGAARGPAG 405

RESULT 4  
US-09-120-601-2  
; Sequence 2, Application US/09120601

Patent No. 6207413  
; GENERAL INFORMATION:  
; APPLICANT: Masiaowski, Piotr  
; TITLE OF INVENTION: No. 6207413el Orphan Receptors  
; FILE REFERENCE: REG 630  
; CURRENT APPLICATION NUMBER: US/09/120,601  
; CURRENT FILING DATE: 1998-07-22  
; EARLIER APPLICATION NUMBER: 09/012,072  
; EARLIER FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: MOUSE  
US-09-120-601-2

Query Match 95.3%; Score 2209; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 5.1e-198;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 SSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGLYWT 80  
Db 1 SSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGLYWT 60  
QY 81 INGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 140  
Db 61 INGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 120  
QY 141 PNISCSNRMDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEBYHTVGPHSCHI 200  
Db 121 PNISCSNRMDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEBYHTVGPHSCHI 180  
QY 201 PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLSVRW 260  
Db 181 PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSRRVGGLEDQLSVRW 240  
QY 261 VSPALPKDFLQAKYQIRYRVEDSVDMKVVDVDSNQTSCRLAGLKEGTYYFVQVRCNPF 320  
Db 241 VSPALPKDFLQAKYQIRYRVEDSVDMKVVDVDSNQTSCRLAGLKEGTYYFVQVRCNPF 300  
QY 321 IYGSKKAGIWSWSHPTAASPRSERPPGGGVCEPRGSGSPVRRBLKDFLWMLKCH 380  
Db 301 IYGSKKAGIWSWSHPTAASPRSERPPGGGVCEPRGSGSPVRRBLKDFLWMLKCH 360  
QY 381 AYCSNLSFRLYDQRAWMOKSHKTRNQDEGILPSGRGAARGPAG 425  
Db 361 AYCSNLSFRLYDQRAWMOKSHKTRNQDEGILPSGRGAARGPAG 405

RESULT 5  
US-09-866-028-32  
; Sequence 32, Application US/09866028  
; Patent No. 6642360  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548PIC1  
; CURRENT APPLICATION NUMBER: US/09/944,457

; FILE REFERENCE: P2548PIC1  
; CURRENT APPLICATION NUMBER: US/09/866,028  
; CURRENT FILING DATE: 2001-05-25  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 32  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-866-028-32

Query Match 93.9%; Score 2176.5; DB 2; Length 422;  
Best Local Similarity 94.8%; Pred. No. 6e-195;  
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;  
QY 1 MPAGRPGPVAQSAARRPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLLQ 60  
Db 1 MPAGRPGPVAQSAARRPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLLQ 57  
QY 61 ATCSIHGDTPGATAEGLYWTINGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120  
Db 58 ATCSVHGDDPPGATAEGLYWTINGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCH 117  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRMDLTCRWTPGAHGETFLHTNYSKYLKRW 180  
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSNRMDLTCRWTPGAHGETFLHTNYSKYLKRW 177  
QY 181 YQDQDNTCEBYHTVGPHSCHI PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTP 240  
Db 178 YQDQDNTCEBYHTVGPHSCHI PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTP 237  
QY 241 PPDVHVSRRVGGLEDQLSVRWVSPALPKDFLQAKYQIRYRVEDSVDMKVVDVDSNQTSCR 300  
Db 238 PPDVHVSRRVGGLEDQLSVRWVSPALPKDFLQAKYQIRYRVEDSVDMKVVDVDSNQTSCR 297  
QY 301 LAGLKEGTYYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSERPPGGGVCEPRGGE 360  
Db 298 LAGLKEGTYYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSERPPGGGVCEPRGGE 357  
QY 361 PSSGVPVRELKDFLWMLKCHAYCSNLSFRLYDQRAWMOKSHKTRNQDEGILPSGRGA 420  
Db 358 PSSGVPVRELKDFLWMLKCHAYCSNLSFRLYDQRAWMOKSHKTRNQDEGILPSGRGA 417  
QY 421 RGPA 424  
Db 418 RGPA 421

RESULT 6  
US-09-944-457-32  
; Sequence 32, Application US/09944457  
; Patent No. 6734288  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548PIC1  
; CURRENT APPLICATION NUMBER: US/09/944,457

RESULT 7  
US-09-945-584-32  
; Sequence 32, Application US/09945584  
; Patent No. 6908993  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivaz  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,584

;  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6908993ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6908993ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000

;  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 32  
; TYPE: PRT  
; LENGTH: 422  
; ORGANISM: Homo Sapien  
; US-09-945-584-32  
  
Query Match 93.9%; Score 2176.5; DB 2; Length 422;  
Best Local Similarity 94.8%; Pred. No. 6e-195;  
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;  
  
QY 1 MPAGRGPPVAQASARPPRLSSIMSPLLICVLGVGRGGGANTAVISPODPTLLIGSSLLQ 60  
Db 1 MPAGRRGPPAAQASARPP-PLLP--LLLCVLGAPRAGSGANTAVISPODPTLLIGSSLL 57  
  
QY 61 ATCSIHGDTPGATAEGLYWTNGRRLLPSLSLLNTSTLALANLNGSRQSGDNLVCH 120  
Db 58 ATCSVHGDPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117  
  
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSNRMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177  
  
QY 181 YGQDNTCEYHTVGHSCHPKDLALFTPYEIVWEATNRLGARSQVLTLDVVTDD 240  
Db 178 YGQDNTCEYHTVGHSCHPKDLALFTPYEIVWEATNRLGARSQVLTLDVVTDD 237  
  
QY 241 PPDVHVSRYGGLLEDOLSVRWVSPPALKDFLQAKYQIRYRVEDSVWKVVDVSNQTSR 300  
Db 238 PPDVHVSRYGGLLEDOLSVRWVSPPALKDFLQAKYQIRYRVEDSVWKVVDVSNQTSR 297  
  
QY 301 LAGLKPGTVYFQVRCNPPGIYGSKKAGIWSWSHPTAASTPRSERPPGGGACEPRGGE 360  
Db 298 LAGLKPGTVYFQVRCNPPGIYGSKKAGIWSWSHPTAASTPRSERPPGGGACEPRGGE 357  
  
QY 361 PSSGVRRELKQFLGWLKKHAYCSNLSFRLYQDQRAWQKSHKTRNQDGLPSGRGAA 420  
Db 358 PSSGVRRELKQFLGWLKKHAYCSNLSFRLYQDQRAWQKSHKTRNQDGLPSGRGAA 417  
  
QY 421 RGPA 424  
Db 418 RGPA 421  
  
RESULT 8  
US-09-944-944-32  
; Sequence 32, Application US/09944944  
; Patent No. 6929947  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Batton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijav, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548PIC1  
; CURRENT APPLICATION NUMBER: US/09/944,944





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; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-071-224-2

Query Match 93.8%; Score 2172.5; DB 2; Length 422;
Best Local Similarity 94.6%; Pred. No. 1.4e-194;
Matches 401; Conservative 6; Mismatches 14; Indels 3; Gaps 2;

Qy 1 MPAGRPGVQAQARRPRRLSSLLVGLVGRGGGAHTAVISPDPTLLIGSSLLQ 60
Db 1 MPAGRRGPAQASRRPP-PLLPLL--LLLCVLGAPRAGGAHTAVISPDPTLLIGSSLL 57
Qy 61 ATCSIHGDPGATAGLYWTLNRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
Db 58 ATCSVHGDPGATAGLYWTLNRRRLPPELSRVINASTLALANLNGSRQSGDNLVCH 117
Qy 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSLKYLKW 180
Db 118 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSLKYLKW 177
Qy 181 YGQDNTCEEYHTVGPHSCHIPKDIALFTPYEIWEATNRLGARSVDLTLVDLVVTTDP 240
Db 178 YGQDNTCEEYHTVGPHSCHIPKDIALFTPYEIWEATNRLGARSVDLTLVDLVVTTDP 237
Qy 241 PPDVHSRVGGLDQLSVRWVSPALKDPLFOAKYQIRYRVEDSVKVVDDVSNQTSR 300
Db 238 PPEVHSRVGGLDQLSVRWVSPALKDPLFOAKYQIRYRVEDSVKVVDDVSNQTSR 297
Qy 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGE 360
Db 298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGE 357
Qy 361 PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRQDEGILPSGRGAA 420
Db 358 PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRQDEGILPSGRGTA 417
Qy 421 RGA 424
Db 418 RGA 421

RESULT 11
US-09-071-224-19
; Sequence 19, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Preenell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.

; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; FILING DATE:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-224-19

Query Match 90.5%; Score 2097; DB 2; Length 385;
Best Local Similarity 99.7%; Pred. No. 1.4e-187;
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 41 AHTAVISPDPTLLIGSSLLQATCSIHGDPGATAGLYWTLNRRRLPSLSRLNTSTLA 100
Db 1 AHTAVISPDPTLLIGSSLLQATCSIHGDPGATAGLYWTLNRRRLPSLSRLNTSTLA 60
Qy 101 LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTP 160
Db 61 LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTP 120
Qy 161 GAHGETFLHTNYSLKYLKWYQDNTCEEYHTVGPHSCHIPKDIALFTPYEIWEATNRL 220
Db 121 GAHGETFLHTNYSLKYLKWYQDNTCEEYHTVGPHSCHIPKDIALFTPYEIWEATNRL 180
Qy 221 GSARSVDLTLVDLVVTTDPPDVHVS RVGGLDQLSVRWVSPALKDPLFOAKYQIRYR 280
Db 181 GSARSVDLTLVDLVVTTDPPDVHVS RVGGLDQLSVRWVSPALKDPLFOAKYQIRYR 240
Qy 281 VEDSDVKVDDVSNQTSRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAAS 340
Db 241 VEDSDVKVDDVSNQTSRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAAS 300
Qy 341 TPRSERPGGGVCEPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQK 400
Db 301 TPRSERPGGGVCEPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQK 360
Qy 401 SHKTRNQDEGILPSGRGAARGPAG 425
Db 361 SHKTRNQDEGILPSGRGAARGPAG 385
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RESULT 12  
US-09-521-335-12  
; Sequence 12, Application US/09521335  
; Patent No. 6800460  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/09/521,335  
; CURRENT FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate  
US-09-521-335-12

Query Match 90.4%; Score 2095; DB 2; Length 410;  
Best Local Similarity 93.9%; Pred. No. 2.4e-187; Indels 6; Gaps 3;  
Matches 388; Conservative 6; Mismatches 13;

QY 1 MPAGRPGVPAQSARRPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSILQ 60  
Db 1 MPAGRPGVPAQSARRPP-PLLP-LLLVLGAPRAGSGAHTAVISPODPTLLIGSSIL 57

QY 61 ATCSIHGDTPGATAGLYWTLNGLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
Db 58 ATCSVHGDPGATAGLYWTLNGLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177

QY 181 YQDNTCEYHTVGPCHSCHI PKDLALFTPEYIWEATNRLGARSDDLTLVDVVTDP 240  
Db 178 YQDNTCEYHTVGPCHSCHI PKDLALFTPEYIWEATNRLGARSDDLTLVDVVTDP 237

QY 241 PPDVHVS RVGGLEDQLSVRWVSPALPKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
Db 238 PPDVHVS RVGGLEDQLSVRWVSPALPKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 297

QY 301 LAGLPGTYVYFVQVRCNPFYIYVSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360  
Db 298 LAGLPGTYVYFVQVRCNPFYIYVSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 357

QY 361 PSSGPVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ 413  
Db 358 PSSGPVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLP 407

RESULT 13  
US-09-071-224-4  
; Sequence 4, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA

COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,224  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-071-224-4

Query Match 90.4%; Score 2094; DB 2; Length 425;  
Best Local Similarity 94.8%; Pred. No. 3.1e-187; Indels 4; Gaps 2;  
Matches 386; Conservative 5; Mismatches 12;

QY 1 MPAGRPGVPAQSARRPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSILQ 60  
Db 1 MPAGRPGVPAQSARRPP-PLLP-LLLVLGAPRAGSGAHTAVISPODPTLLIGSSIL 56

QY 61 ATCSIHGDTPGATAGLYWTLNGLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 120  
Db 57 ATCSVHGDPGATAGLYWTLNGLRPLSELRLNTSTLALANLNGSRQSGDNLVCH 116

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
Db 117 ARDGSILAGSCLYVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176

QY 181 YQDNTCEYHTVGPCHSCHI PKDLALFTPEYIWEATNRLGARSDDLTLVDVVTDP 240  
Db 177 YQDNTCEYHTVGPCHSCHI PKDLALFTPEYIWEATNRLGARSDDLTLVDVVTDP 236

QY 241 PPDVHVS RVGGLEDQLSVRWVSPALPKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300  
Db 237 PPDVHVS RVGGLEDQLSVRWVSPALPKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 296

QY 301 LAGLPGTYVYFVQVRCNPFYIYVSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360  
Db 297 LAGLPGTYVYFVQVRCNPFYIYVSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 356

QY 361 PSSGPVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ 407  
Db 357 PSSGPVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ 403

RESULT 14  
US-09-120-601-6  
; Sequence 6, Application US/09120601  
; Patent No. 6207413  
; GENERAL INFORMATION:  
; APPLICANT: Masiakowski, Piotr  
; TITLE OF INVENTION: No. 6207413el Orphan Receptors  
; FILE REFERENCE: REG 630

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; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 448
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-6

Query Match      89.4%; Score 2071.5; DB 2; Length 448;
Best Local Similarity 90.0%; Pred. No. 4.3e-185;
Matches 386; Conservative 5; Mismatches 13; Indels 25; Gaps 3;

QY 1 MPAGRPGPVAQARPPRLSSILWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIIQ 60
DB 1 MPAGRGPAAQARPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSII 57
QY 61 ATCSIHGDPGATAEGLYWTNGRRLPSELRLNLTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGATAEGLYWTNGRRLPSELRLNLTSTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWSNMKDLTCRWTPGAHGETFLHTNYSCLKYLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWSNMKDLTCRWTPGAHGETFLHTNYSCLKYLRW 177
QY 181 YGQDNTCEHYHTVGHPSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDVID----- 234
DB 178 YGQDNTCEHYHTVGHPSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDIDVGSHP 237
QY 235 -----VTTDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQIR 278
DB 238 LPSPATPGLSLLVRGKVTTDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQIR 297
QY 279 YRVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPTA 338
DB 298 YRVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPTA 357
QY 339 ASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 398
DB 358 ASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 417
QY 399 QKSHKTRNQ 407
DB 418 QKSHKTRNQ 426
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RESULT 15
US-09-071-224-17
; Sequence 17, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-224-17

Query Match      88.5%; Score 2051; DB 2; Length 388;
Best Local Similarity 96.4%; Pred. No. 2.9e-183;
Matches 373; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 38 GSGAHTAVISPODPTLLIGSSIIQATCSIHGDPGATAEGLYWTNGRRLPSELRLNLT 97
DB 1 GSGAHTAVISPODPTLLIGSSIIATCSVHGDPGATAEGLYWTNGRRLPSELRLNAS 60
QY 98 TLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLPPEKPNISCSWSNMKDLTCR 157
DB 61 TLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLPPEKPNISCSWSNMKDLTCR 120
QY 158 WTPGAHGETFLHTNYSCLKYLRWYQDNTCEHYHTVGHPSCHIPKDLALFTPEYIWEAT 217
DB 121 WTPGAHGETFLHTNYSCLKYLRWYQDNTCEHYHTVGHPSCHIPKDLALFTPEYIWEAT 180
QY 218 NRLGARSVDLTLDVLDVTTDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQI 277
DB 181 NRLGARSVDLTLDVLDVTTDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQI 240
QY 278 YRVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPT 337
DB 241 YRVEDSVDMKVVDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPT 300
QY 338 AASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 397
DB 301 AASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 360
QY 398 MOKSHKTRNQDEGILPSGRGARGPA 424
DB 361 MOKSHKTRNQDEGILPSGRGARGPA 387
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Search completed: April 11, 2006, 02:18:58  
Job time : 30.3685 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:03:38 ; Search time 115.031 Seconds  
(without alignments)  
1608.075 Million cell updates/sec

Title: US-09-037-657-44

Perfect score: 2290

Sequence: 1 MPAGRRGPAQAARPPPL.....NODEGILPSRRGTARGPAR 421

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2290	100.0	421	4	Aae00826 Murine ha
2	2279.5	99.5	422	2	Aay05782 Human typ
3	2279.5	99.5	422	2	Aay06479 Human tum
4	2279.5	99.5	422	2	Aay17825 Human PRO
5	2279.5	99.5	422	2	Aay26339 Human U4
6	2279.5	99.5	422	3	Aab01316 Human PRO
7	2279.5	99.5	422	3	Aay93686 Amino aci
8	2279.5	99.5	422	4	Agg63545 Amino aci
9	2279.5	99.5	422	6	Abu55925 Human sec
10	2279.5	99.5	422	6	Abu60235 Human PRO
11	2279.5	99.5	422	6	Abg72776 Human cyt
12	2279.5	99.5	422	6	Abu64921 Human sec
13	2279.5	99.5	422	6	Abu58355 Novel hum
14	2279.5	99.5	422	6	Abu57241 Human PRO
15	2279.5	99.5	422	6	Abu56306 Human sec
16	2279.5	99.5	422	6	Abu60346 Novel hum
17	2279.5	99.5	422	6	Abu11307 Human pro
18	2279.5	99.5	422	6	Abu67126 Human PRO
19	2279.5	99.5	422	7	Adc25788 Human sec
20	2279.5	99.5	422	7	Adc25546 Human sec
21	2279.5	99.5	422	7	Adc25667 Human sec
22	2279.5	99.5	422	7	Adh27452 Human sec
23	2279.5	99.5	422	8	Adh71501 Human sec
24	2279.5	99.5	422	8	Adg63444 Human sec

25	2279.5	99.5	422	8	ADH43173 Human sec
26	2279.5	99.5	422	8	ADN04232 Antipsori
27	2279.5	99.5	422	8	ADN00411 Human sec
28	2279.5	99.5	422	8	ADQ18851 Human sof
29	2279.5	99.5	422	8	ADU06568 Novel bro
30	2279.5	99.5	422	8	ADU25335 Human sec
31	2279.5	99.5	422	9	ADY39498 Human PRO
32	2279.5	99.5	422	9	ADY73779 Human PRO
33	2275.5	99.4	422	2	AAW70860 Human ZCY
34	2208.5	96.4	408	2	AAW59805 Amino aci
35	2208.5	96.4	408	2	AAV26338 Human U4
36	2208.5	96.4	408	2	ADRA41505 Human CD-
37	2196	95.9	425	2	AAW70861 Allelic v
38	2188	95.5	410	2	AAY29779 Human DNA
39	2188	95.5	410	3	AAB19588 Human cyt
40	2188	95.5	410	4	AAB36647 Human cyt
41	2188	95.5	410	7	ADC07179 Human cyt
42	2188	95.5	410	8	ADT90844 Human cyt
43	2188	95.5	410	8	ADT61032 Human cyt
44	2188	95.5	410	9	ADY57157 Human cyt
45	2188	95.5	410	9	ADZ65014 Human NR6

#### ALIGNMENTS

##### RESULT 1

AAE00826

ID AAE00826 standard; protein; 421 AA.

AC AAE00826;

DT 09-SEP-2004 (revised)

DT 02-JUL-2001 (first entry)

XX

XX Murine haemopoietin receptor, NR6 protein, encoded by NR6 DNA.

DE Murine; biologically active complex; haemopoietin receptor; NR6;

KW cardiostrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;

XX differentiation; cell survival; neurotrophic activity.

XX Mus sp.

OS Unidentified.

XX WO200127157-A1.

XX 19-APR-2001.

XX

PF 06-OCT-2000; 2000WO-AU001216.

XX

XX 08-OCT-1999; 99AU-00003327.

PR 12-MAY-2000; 2000AU-00007489.

XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX

PI Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PP, Hilton DJ;

XX Nakata Y, Hasegawa M;

XX

DR WPI; 2001-281978/29.

XX

DR N-PSDB; AAD04199.

XX

PT New biologically active complex comprising NR6 and cardiostrophin-like-

XX cytokine, for facilitating proliferation, differentiation and/or survival

XX

XX Claim 29; Page 106-107; 123pp; English.

XX

CC The present invention relates to a biologically active complex comprising

CC a haemopoietin receptor, NR6 and cardiostrophin-like cytokine (CLC). The

CC complex is useful in the manufacture of a medicament for the treatment

CC and/or prophylaxis of a subject, as it is involved in facilitating

CC proliferation, differentiation and/or survival of a cell. The complex or

CC its components have neurotrophic activity. The present sequence is murine

CC

```
CC haemopoietin receptor, NR6 protein, encoded by NR6 DNA
CC Revised record issued on 09-SEP-2004 : Correction to Organism field
XX SQ Sequence 421 AA;
Query Match 100.0%; Score 2290; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.1e-185; Indels 0; Gaps 0;
Matches 421; Conservative 0; Mismatches 0;
QY 1 MPAGRRGPAQAQARRPPPLP LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS 60
DB 1 MPAGRRGPAQAQARRPPPLP LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS 60
QY 61 VHGDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120
DB 61 VHGDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120
QY 121 SILAGSCLYVGLPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 180
DB 121 SILAGSCLYVGLPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 180
QY 181 NTCEBYHTVGPCHSCHIPKD LALFTPYEIWVEATNRLGARSVDLTLDILDVVTTDPPDV 240
DB 181 NTCEBYHTVGPCHSCHIPKD LALFTPYEIWVEATNRLGARSVDLTLDILDVVTTDPPDV 240
QY 241 HVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDWKVVDDVSNQTSRLAGL 300
DB 241 HVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDWKVVDDVSNQTSRLAGL 300
QY 301 KPGTVYFVQVRCNPFGIYVSKKAGIWSWSHPTAATPSRPPGPGGACPRGGEPSGG 360
DB 301 KPGTVYFVQVRCNPFGIYVSKKAGIWSWSHPTAATPSRPPGPGGACPRGGEPSGG 360
QY 361 PVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSSRGRTARGPA 420
DB 361 PVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSSRGRTARGPA 420
QY 421 R 421
DB 421 R 421
RESULT 2
ID AAY05782
XX AAY05782 standard; protein; 422 AA.
AC AAY05782;
XX AAY05782;
DT 02-AUG-1999 (first entry)
DE Human type 1 cytokine receptor GBRI-ILR.
XX GBRI-ILR; hGBR-ILR; cytokine receptor; human; cancer; obesity;
KW inflammation; septic shock; AIDS; embryo development; lung infection;
KW cytostatic; anorectic; immunosuppressive; antibacterial; antiviral;
KW antiinflammatory; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..37
FT /note= "signal peptide"
FT Protein 38..422
FT /note= "mature protein; a polypeptide comprising amino
FT acids 38-422 is also claimed in Claim 1a"
XX
XX WO9920755-A2.
XX
XX 29-APR-1999.
XX
XX 14-OCT-1998; 98WO-EP006497.
XX
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PR 16-OCT-1997; 97GB-00021961.
XX (GLAX ) GLAXO GROUP LTD.
XX Elson G, Gauchat J, Kosco-Vilbois M;
XX WPI; 1999-288305/24.
XX N-PSDB; AAX25489.
PT Novel human or mouse type I cytokine receptors hGBRI-ILR or mGBRI-ILR,
FT useful for treating e.g. cancer, immune disorders, obesity and AIDS.
XX Claim 1a; Fig 4; 41pp; English.
XX The present sequence represents a novel type 1 cytokine receptor that has
CC been termed human GBRI-ILR as it is believed to be an interleukin
CC receptor, or at least a substantial part of such a receptor. The sequence
CC is predicted from an isolated full-length cDNA clone (see AAX25489)
CC obtained from a human placental cDNA library. GBRI-ILR mRNA is expressed
CC most strongly in spleen, thymus, lymph node, appendix, bone marrow,
CC thymoid, adrenal cortex, stomach, heart, placenta and skeletal muscle,
CC suggesting a role for GBRI-ILR in the immune system. In human foetal
CC tissue, strong expression is seen in the lung, but not in brain, kidney
CC or liver. A GBRI-ILR receptor has also been identified in mice (see
CC AAY05783). The high degree of conservation of amino acids between the
CC human and murine polypeptides indicates that this receptor is
CC functionally important. GBRI-ILR polypeptides, nucleic acids, antibodies,
CC agonists and antagonists can be used to treat e.g. cancer, immune
CC disorders, obesity (in view of homology to the leptin receptor),
CC embryonic developmental disorders, AIDS, septic shock and lung infection
CC (claimed)
XX SQ Sequence 422 AA;
Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLP LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 59
DB 1 MPAGRRGPAQAQARRPPPLP LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
QY 60 SVHGDDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
DB 61 SVHGDDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQ 179
DB 121 GSILAGSCLYVGLPPEKPNVISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQ 180
QY 180 DNTCEBYHTVGPCHSCHIPKD LALFTPYEIWVEATNRLGARSVDLTLDILDVVTTDPPD 239
DB 181 DNTCEBYHTVGPCHSCHIPKD LALFTPYEIWVEATNRLGARSVDLTLDILDVVTTDPPD 240
QY 240 VHSVSVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDWKVVDDVSNQTSRLAG 299
DB 241 VHSVSVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDWKVVDDVSNQTSRLAG 300
QY 300 LKPGTVYFVQVRCNPFGIYVSKKAGIWSWSHPTAATPSRPPGPGGACPRGGEPSG 359
DB 301 LKPGTVYFVQVRCNPFGIYVSKKAGIWSWSHPTAATPSRPPGPGGACPRGGEPSG 360
QY 360 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSSRGRTARGP 419
DB 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSSRGRTARGP 420
QY 420 AR 421
DB 421 AR 422
RESULT 3
AAY06479
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ID AAY06479 standard; protein; 422 AA.  
 AC AAY06479;  
 DT 27-SEP-1999 (first entry)  
 DE Human tumour-associated protein PRO327.  
 DE Human tumour-associated protein PRO327.  
 KW PRO327; UNQ288; cancer; tumour; diagnosis; therapy; human.  
 OS Homo sapiens.  
 OS Homo sapiens.  
 PN W09935170-A2.  
 PD 15-JUL-1999.  
 PD 15-JUL-1999.  
 PF 05-JAN-1999; 99WO-US000106.  
 PF 05-JAN-1999; 99WO-US000106.  
 PR 05-JAN-1998; 98US-0070440P.  
 PR 29-APR-1998; 98US-0083500P.  
 PR 22-MAY-1998; 98US-0086414P.  
 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-NOV-1998; 98US-0107783P.  
 PR 20-NOV-1998; 98US-0109304P.  
 XX (GETH ) GENENTECH INC.  
 XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;  
 PI Wood WI;  
 XX WPI; 1999-430385/36.  
 DR N-PSDB; AAX87256.  
 XX Antibody against proteins expressed in neoplastic cells, useful for tumor  
 PT diagnosis and treatment.  
 PT diagnosis and treatment.  
 XX Example 1; Fig 6; 162pp; English.  
 XX This sequence represents human PRO327 (UNQ288), a 46.3 kDa protein (pI  
 CC 9.42) encoded by the novel cDNA clone DNA38113 (see AAX87256).  
 CC Amplification of DNA38113 occurs in various lung and colon tumours and  
 CC cell lines, suggesting a significant role in tumour formation and growth.  
 CC Antagonists (e.g. antibodies) directed against PRO327 are expected to  
 CC have utility in cancer therapy. The invention identifies 14 genes (see  
 CC AAX87254-67) that are amplified in the genome of tumour cells. Such  
 CC amplification is expected to be associated with overexpression of the  
 CC gene product and to contribute to tumorigenesis. The encoded proteins  
 CC (see AAY06477-90) may be useful targets for the diagnosis and/or  
 CC treatment (including prevention) of certain cancers, and may act as  
 CC predictors of the prognosis of tumour treatment. Antibodies that bind the  
 CC proteins are claimed and used in claimed cancer diagnostic kits  
 XX Sequence 422 AA;  
 SQ

Query Match 99.5%; Score 2279.5; DB 2; Length 422;  
 Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MPAGRRGPAQAQARRPPPLP-LLLCVLGAPRAGAGTAIVISPDPTLLIGSSLLATC 59  
 Db 1 MPAGRRGPAQAQARRPPPLP-LLLCVLGAPRAGAGTAIVISPDPTLLIGSSLLATC 60  
 QY 60 SVHGDPPGATAGLYWTNGRLRPPELSRVINASTLALANLNGSRQSGDNLVCHARD 119  
 Db 61 SVHGDPPGATAGLYWTNGRLRPPELSRVINASTLALANLNGSRQSGDNLVCHARD 120  
 QY 120 GSILAGSLYVLGPPKPNVISCWKNMDLTCRWTPGAHGETFLHTNYSLKYLKWYQ 179  
 Db 121 GSILAGSLYVLGPPKPNVISCWKNMDLTCRWTPGAHGETFLHTNYSLKYLKWYQ 180  
 QY 180 DNTCEYHTVGHSCHPKDLALFTPEIWEATNRLGARSVDLFLDLDVVTTDPPPD 239  
 Db 181 DNTCEYHTVGHSCHPKDLALFTPEIWEATNRLGARSVDLFLDLDVVTTDPPPD 240

QY 240 VHVSRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 299  
 XX |||||  
 Db 241 VHVSRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 300  
 XX |||||  
 QY 300 LKPGTYVYFQVRCNPFYIYGSKKAGIWSWSHPTAASPRSRPFGGGGACBPRGGPSS 359  
 XX |||||  
 Db 301 LKPGTYVYFQVRCNPFYIYGSKKAGIWSWSHPTAASPRSRPFGGGGACBPRGGPSS 360  
 XX |||||  
 QY 360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDSGILPSGRRGTARGP 419  
 XX |||||  
 Db 361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDSGILPSGRRGTARGP 420  
 XX |||||  
 QY 420 AR 421  
 XX ||  
 Db 421 AR 422  
 XX ||  
 RESULT 4  
 AAY17825  
 ID AAY17825 standard; protein; 422 AA.  
 XX AAY17825;  
 AC AAY17825;  
 XX 12-AUG-1999 (first entry)  
 DT 12-AUG-1999 (first entry)  
 DE Human PRO327 protein sequence.  
 DE Human PRO327 protein sequence.  
 XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;  
 KW secreted protein; transmembrane protein; inflammation disorder.  
 KW secreted protein; transmembrane protein; inflammation disorder.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 OS Homo sapiens.  
 PN W09928462-A2.  
 PD 10-JUN-1999.  
 PD 10-JUN-1999.  
 PF 01-DEC-1998; 98WO-US025108.  
 PF 01-DEC-1998; 98WO-US025108.  
 PR 03-DEC-1997; 97US-0067411P.  
 PR 11-DEC-1997; 97US-0069278P.  
 PR 11-DEC-1997; 97US-0069334P.  
 PR 11-DEC-1997; 97US-0069335P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 16-DEC-1997; 97US-0069694P.  
 PR 16-DEC-1997; 97US-0069696P.  
 PR 16-DEC-1997; 97US-0069702P.  
 PR 17-DEC-1997; 97US-0069870P.  
 PR 17-DEC-1997; 97US-0069873P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 05-JAN-1998; 98US-0070440P.  
 PR 09-FEB-1998; 98US-0074086P.  
 PR 09-FEB-1998; 98US-0074092P.  
 PR 25-FEB-1998; 98US-0075945P.  
 XX (GETH ) GENENTECH INC.  
 PA (GETH ) GENENTECH INC.  
 XX Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;  
 XX WPI; 1999-371118/31.  
 DR N-PSDB; AAX80050.  
 XX Nucleic acids encoding PRO secreted and transmembrane proteins.  
 PT Nucleic acids encoding PRO secreted and transmembrane proteins.  
 PS Claim 12; Fig 17; 123pp; English.  
 XX The present invention describes nucleic acids encoding PRO secreted and  
 CC transmembrane proteins used therapeutically. The PRO proteins have  
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive  
 CC activity. The proteins and polynucleotides can be used in therapy,  
 CC identification of homologues, raising antibodies and design of probes and  
 CC primers. They can be used in a range of diseases related to proteins that  
 CC they have homology with, e.g. a PRO protein having homology to complement







XX	Homo sapiens.	
XX	WO200155172-A2.	
XX	02-AUG-2001.	
XX	26-JAN-2001; 2001WO-FR000253.	
XX	27-JAN-2000; 2000FR-00001035.	
XX	12-OCT-2000; 2000FR-00013089.	
XX	(FABR ) FABRE MEDICAMENT SA PIERRE.	
XX	(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.	
XX	Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;	
XX	WPI; 2001-488773/53.	
XX	N-PSDB; AAH74486.	
XX	A complex comprising a NNT-1 protein and a CLF-1 and/or scNTRalpha	
XX	protein useful to treat neurodegenerative disease including Parkinson's	
XX	and Huntington's, obesity and cancer.	
XX	Claim 2; Page 63-64; 67pp; French.	
XX	The present sequence represents a human CLF-1 protein. The specification	
XX	describes a complex comprising a NNT-1 protein and a CLF-1 and/or	
XX	scNTRalpha protein. The NNT-1/CLF-1 complex is used to modulate activity	
XX	of the scNTRalpha/gpi30/LiFRbeta receptor complex, or to induce	
XX	phosphorylation of the tyrosine of gpi30 and LiFRbeta, particularly where	
XX	cells expressing the receptor complex are in the central or peripheral	
XX	nervous system, in neurons implicated in neuro-muscular function or in	
XX	skeletal muscle. The complex or antibodies are also used to decrease the	
XX	survival, growth or proliferation of tumour cells or to facilitate the	
XX	proliferation and/or inhibit differentiation of cells stocks. The complex	
XX	is also used to modulate activity of the gpi30/LiFRbeta receptor or cells	
XX	expressing that receptor, particularly those cells implicated in the	
XX	immune, haematopoietic, nervous or reproductive system, the liver or	
XX	skeletal muscle. Molecules of the invention may be used to prevent or	
XX	treat neurodegenerative diseases including amyotrophic lateral sclerosis,	
XX	Parkinson's and Huntington's disease, to repair or regenerate nervous or	
XX	muscular tissue or to maintain muscular mass in paralysis patients. They	
XX	may also be used to treat cancer, obesity and associated diseases, and to	
XX	improve fertility, particularly to avoid endometriosis and/or assist	
XX	blastocyst implantation, thrombosis, or retinal disease, particular	
XX	retinal pigmentosis	
XX	Sequence 422 AA;	
XX	Query Match	
XX	Best Local Similarity 99.5%; Score 2279.5; DB 4; Length 422;	
XX	Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	
QY	1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISQDPPTLLTGSSLLATC 59	
Db	1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISQDPPTLLTGSSLLATC 60	
QY	60 SVHGDDPGATAGLWTLNGLRPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119	
Db	61 SVHGDDPGATAGLWTLNGLRPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120	
QY	120 GSILAGSCLYGLPEKPNVISCWKNMKDLTCRWTPGAGHGETFLHTNYSKYKLRWYGO 179	
Db	121 GSILAGSCLYGLPEKPNVISCWKNMKDLTCRWTPGAGHGETFLHTNYSKYKLRWYGO 180	
QY	180 DNTCEYHTVGHSHCHIPKDLALFTPYEIVWEATNRLASARSDVLTLDLDVTTDPPPD 239	
Db	181 DNTCEYHTVGHSHCHIPKDLALFTPYEIVWEATNRLASARSDVLTLDLDVTTDPPPD 240	
QY	240 VHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAG 299	
Db	241 VHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAG 300	
QY	300 LKPGTVYFVQVRCNPFGIYGSKAGIWSHPTAASRPRSGPGGACPRGCEPSS 359	
Db	301 LKPGTVYFVQVRCNPFGIYGSKAGIWSHPTAASRPRSGPGGACPRGCEPSS 360	
QY	360 GPNRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDSGILPSSRRGTARGP 419	
Db	361 GPNRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDSGILPSSRRGTARGP 420	
QY	420 AR 421	
Db	421 AR 422	
XX	RESULT 9	
XX	ABU55925	
XX	ID ABU55925 standard; protein; 422 AA.	
XX	AC ABU55925;	
XX	XX 26-MAR-2003 (first entry)	
XX	DE Human secreted/transmembrane protein PRO327.	
XX	XX Human; PRO; secreted protein; transmembrane protein; anti-HIV;	
XX	KW cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic;	
XX	KW cardiac; AIDS; acquired immunodeficiency syndrome; cancer;	
XX	KW atherosclerosis; inflammatory disease; diabetic complication;	
XX	XX cardiac injury; organ failure.	
XX	OS Homo sapiens.	
XX	PN US2002142959-A1.	
XX	PD 03-OCT-2002.	
XX	XX 31-AUG-2001; 2001US-00944654.	
XX	PR 16-SEP-1998; 98WO-US019330.	
XX	PR 01-DEC-1998; 98WO-US025108.	
XX	PR 22-JUN-1999; 99WO-US012252.	
XX	PR 15-SEP-1999; 99WO-US021090.	
XX	PR 30-NOV-1999; 99WO-US028313.	
XX	PR 30-NOV-1999; 99WO-US028409.	
XX	PR 01-DEC-1999; 99WO-US028301.	
XX	PR 16-DEC-1999; 99WO-US030095.	
XX	PR 11-FEB-2000; 2000WO-US003565.	
XX	PR 22-FEB-2000; 2000WO-US004114.	
XX	PR 02-MAR-2000; 2000WO-US005841.	
XX	PR 30-MAR-2000; 2000WO-US008439.	
XX	PR 22-MAY-2000; 2000WO-US014042.	
XX	PR 28-JUL-2000; 2000WO-US020710.	
XX	PR 01-DEC-2000; 2000WO-US032678.	
XX	PR 28-FEB-2001; 2001WO-US006520.	
XX	PR 25-MAY-2001; 2001US-00866028.	
XX	(GETH ) GENENTECH INC.	
XX	Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;	
XX	PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;	
XX	PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;	
XX	XX WPI; 2003-174141/17.	
XX	DR N-PSDB; ABX75462.	
XX	XX New isolated PRO polypeptide and encoding nucleic acid, useful for the	
XX	PT diagnosis and treatment of disorders associated with the PRO polypeptide,	
XX	PT such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.	
XX	PS Claim 12; Fig 14; 178pp; English.	
XX	XX The invention relates to an isolated PRO polypeptide (a secreted or	
XX	CC transmembrane protein) comprising: (a) at least 80% sequence identity or	

CC positives when compared to any of 15 sequences, fully defined in the  
CC specification, lacking or with its associated signal peptide; or (b) at  
CC least 80% sequence identity to a sequence encoded by the full-length  
CC coding sequence of a DNA deposited in the American Type Culture  
CC Collection (ATCC). Also included are: (1) an isolated nucleic acid  
CC comprising: (a) at least 80% sequence identity to a nucleotide sequence  
CC that encodes a PRO protein; (b) at least 80% sequence identity to a  
CC nucleotide sequence or full-length coding sequence with any of 15 fully  
CC defined sequences of 957-3441 base pairs, given in the specification; or  
CC (c) at least 80% sequence identity to a full-length coding sequence of a  
CC DNA deposited under ATCC Accession No. 209526, 209508, 209524, 209528,  
CC 209530, 209523, 209432, 209532, 209531, 209529, 209527, 209570, 209618,  
CC 209621 or 209619; (2) a vector comprising the nucleic acid; (3) a host  
CC cell comprising the vector which, when cultured under conditions suitable  
CC for expression of the PRO polypeptide, produces the PRO protein; (4) a  
CC chimeric molecule comprising PRO fused to a heterologous amino acid  
CC sequence; and (5) an anti-PRO antibody. The methods and compositions of  
CC the present invention are useful for the diagnosis and treatment of  
CC disorders associated with the PRO polypeptide, such as AIDS (acquired  
CC immunodeficiency syndrome), cancer, atherosclerosis, inflammatory  
CC disease, diabetic complications, cardiac injury and organ failure. The  
CC antibodies can also be used in the different screening, therapeutic and  
CC biological assays. The present sequence represents a PRO protein  
XX  
SQ Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;  
Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSAGTAIVISPDPTLLIGSSLLATC 59  
Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSAGTAIVISPDPTLLIGSSLLATC 60

QY 60 SVHGPPPGATAGLYWTLNGRLPPPELSRVLANASTLALANLNGSRQSGNVLVCHARD 119  
Db 61 SVHGPPPGATAGLYWTLNGRLPPPELSRVLANASTLALANLNGSRQSGNVLVCHARD 120

QY 120 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHETFLHTNYSLKYLRYWYQ 179  
Db 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHETFLHTNYSLKYLRYWYQ 180

QY 180 DNTCEYHTVGHSHCHIPKDLALFTPEYIWEATNRLGARSDDLTLIDVVTDDPPD 239  
Db 181 DNTCEYHTVGHSHCHIPKDLALFTPEYIWEATNRLGARSDDLTLIDVVTDDPPD 240

QY 240 VHSRVYGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDWKVDDVSNQTSCLLAG 299  
Db 241 VHSRVYGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDWKVDDVSNQTSCLLAG 300

QY 300 LKPGTYVYFVQRCNPFYIGSKKAGIWSWSHPTAATPRSERPGGGACPRGGEPS 359  
Db 301 LKPGTYVYFVQRCNPFYIGSKKAGIWSWSHPTAATPRSERPGGGACPRGGEPS 360

QY 360 GPVRRLEKQFLGWLKHAHCNSLSPFLYDQRAWMOKSHKTRNQDGIILPSGRGTARGP 419  
Db 361 GPVRRLEKQFLGWLKHAHCNSLSPFLYDQRAWMOKSHKTRNQDGIILPSGRGTARGP 420

QY 420 AR 421  
Db 421 AR 422

RESULT 10  
ABU60235  
ID ABU60235 standard; protein; 422 AA.  
XX  
AC ABU60235;  
XX  
DT 24-APR-2003 (first entry)  
XX  
DE Human PRO polypeptide #6.  
XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer;  
KW inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility;  
KW birth defect; premature aging; diabetes; dog; cat; horse;  
KW acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit;  
KW industry; cytostatic; antiinflammatory; cardiant; antinfertility;  
KW anti-HIV; antiarteriosclerotic; antidiabetic.  
XX  
OS Homo sapiens.  
XX  
PN US2002132768-A1.  
XX 19-SEP-2002.  
XX 31-AUG-2001; 2001US-00945015.  
XX 03-DEC-1997; 97US-0067411P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 16-DEC-1997; 97US-0069696P.  
PR 16-DEC-1997; 97US-0069702P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 17-DEC-1997; 97US-0069873P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 05-JAN-1998; 98US-0070440P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 01-DEC-1998; 98WO-US025108.  
PR 16-DEC-1998; 98US-00216021.  
PR 16-DEC-1998; 98US-0112850P.  
PR 22-DEC-1998; 98US-00218517.  
PR 22-DEC-1998; 98US-0113296P.  
PR 03-MAR-1999; 99US-00254311.  
PR 22-JUN-1999; 99WO-US012252.  
PR 28-JUL-1999; 99US-0146222P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff B;  
PI Gerritsen ME, Goddard AJ, Godowski FJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, KJlavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX  
DR WPI; 2003-174088/17.  
DR N-PSDB; ABX89453.  
XX  
PT New secreted and transmembrane polypeptides (e.g. PRO241, for use in  
PT pharmaceuticals, diagnostics or bioreactors, particularly for detecting  
PT or treating e.g. cancers, infertility or acquired immunodeficiency  
PT syndrome in mammals.  
XX  
PS Claim 1; Fig 14; 173pp; English.  
XX  
CC The invention relates to a human secreted and transmembrane polypeptide  
CC (PRO) and the polynucleotide encoding it. The PRO polypeptide or  
CC polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or

CC bioreactors. These are particularly useful for detecting or treating  
CC cancers, inflammatory diseases, atherosclerosis, cardiac injury,  
CC infertility, birth defects, premature aging, acquired immunodeficiency  
CC syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,  
CC cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are  
CC also useful in biotechnological and medical research and in various  
CC industrial applications. Sequences ABU60230-ABU60245 represent human PRO  
CC polypeptides of the invention  
XX  
SQ Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;  
Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59  
DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60  
QY 60 SVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119  
DB 61 SVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120  
QY 120 GSILAGSCLYVGLPPEKPNISCSKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 179  
DB 121 GSILAGSCLYVGLPPEKPNISCSKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 180  
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSDDLTLDDVVTTDPPD 239  
DB 181 DNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSDDLTLDDVVTTDPPD 240  
QY 240 VHVSRVGGLEDQLSVRWVFPFALKDQFQAKYQIRYRVEDSDVKWVDVDSNQTSCRLAG 299  
DB 241 VHVSRVGGLEDQLSVRWVFPFALKDQFQAKYQIRYRVEDSDVKWVDVDSNQTSCRLAG 300  
QY 300 LKPGTVYFVQRCNPGIYSGKAGIWSWSHPTAATPRSRPSPGGGACPRGEPSS 359  
DB 301 LKPGTVYFVQRCNPGIYSGKAGIWSWSHPTAATPRSRPSPGGGACPRGEPSS 360  
QY 360 GVPRELKQFLGWLKHKHAYCSNLSFELYDQWAWQSHKTNQDEGILPSSRRGTARGP 419  
DB 361 GVPRELKQFLGWLKHKHAYCSNLSFELYDQWAWQSHKTNQDEGILPSSRRGTARGP 420  
QY 420 AR 421  
DB 421 AR 422

## RESULT 11

ABG72776  
ID ABG72776 standard; protein; 422 AA.

XX AC ABG72776;

XX DT 20-FEB-2003 (first entry)

XX DE Human cytokine receptor-like factor 1 (CLF-1 or CLRF-1) protein.

XX KW Human; gene expression; bone formation; cartilage formation;  
KW embryonic development; cytokine receptor-like factor 1; CLF-1; CLRF-1;  
KW mesenchymal cell differentiation; matrix metalloproteinase 23; MMP23;  
KW bone development; antagonist; agonist; cadherin; CD68; cytokine;  
KW diagnosis; osteodystrophy; osteohypertrophy; osteoblastoma;  
KW osteopetrosis; osteogenesis imperfecta; osteoporosis; osteopenia;  
KW osteoma; osteoblastoma; periodontal disease; hyperparathyroidism;  
KW hypercalcaemia of malignancy; Paget's disease; osteolytic lesion;  
KW bone metastasis; bone loss; immobilisation; sex hormone deficiency;  
KW inflammatory disease; rheumatoid arthritis; osteoarthritis;  
KW bone fracture.

XX OS Homo sapiens.

XX WO200285285-A2.

PN

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012149.

XX 18-APR-2001; 2001US-0284786P.

XX (AMHP ) WYETH.

XX Clancy B, Pittman DM;

XX WPI: 2003-103384/09.

XX N-PSDB; ABX14013.

PT Determining the difference between levels of expression of a number of  
PT genes, useful for diagnosing and treating disorders associated with bone  
PT or cartilage formation or resorption such as osteoporosis and bone  
PT fractures.

PS Disclosure; Page 192-193; 197pp; English.

XX The invention discloses a method for determining the difference between  
XX the levels of expression of a number of, at least 500 genes, during bone  
XX or cartilage formation. The method comprises determining levels of RNA  
XX from the genes to obtain levels of expression and comparing these to a  
XX set of reference levels for each of the genes. Bone formation is an  
XX essential process in embryonic development and plays a critical role in  
XX many diseases and conditions in humans. Two genes found to be regulated  
XX during bone and cartilage formation are the cytokine receptor-like factor  
XX 1 (CLF-1 or CLRF-1), which is specifically regulated during mesenchymal  
XX cell differentiation, and matrix metalloproteinase 23 (MMP23), which is  
XX specifically regulated during bone development. Also disclosed is a  
XX computer program for analysing levels of expression of a number of genes,  
XX compositions comprising a number of antagonists or agonists of the genes  
XX and methods for determining whether a subject has, or is likely to  
XX develop, a disease related to bone or cartilage resorption or formation,  
XX for determining the effectiveness of a treatment intended to stimulate  
XX bone or cartilage formation or resorption, for identifying a compound for  
XX treating, modulating or stimulating a disease related to bone or  
XX cartilage formation possibly acting as a cadherin or CD68 agonist or a  
XX cytokine antagonist. The methods and compositions are useful for  
XX diagnosing and treating disorders associated with bone or cartilage  
XX formation or resorption such as osteodystrophy, osteohypertrophy,  
XX osteoblastoma, osteopetrosis, osteogenesis imperfecta, osteoporosis,  
XX osteopenia, osteoma and osteoblastoma, periodontal disease,  
XX hyperparathyroidism, hypercalcaemia of malignancy, Paget's disease,  
XX osteolytic lesions produced by bone metastasis, bone loss due to  
XX immobilisation or sex hormone deficiency, bone and cartilage loss caused  
XX by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone  
XX fractures. The sequence presented is the human CLF-1 protein

XX Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;  
Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59  
DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60  
QY 60 SVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119  
DB 61 SVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120  
QY 120 GSILAGSCLYVGLPPEKPNISCSKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 179  
DB 121 GSILAGSCLYVGLPPEKPNISCSKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 180  
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSDDLTLDDVVTTDPPD 239  
DB 181 DNTCEYHTVGPHSCHIPKDLALFTPEIWEATNRLGARSDDLTLDDVVTTDPPD 240

QY 240 VHSVGVGLEDQLSVRWVSPPALKDPLFOAKYQIRYRVSDSVDMKVVDDVSNQTSCLAG 299  
Db 241 VHSVGVGLEDQLSVRWVSPPALKDPLFOAKYQIRYRVSDSVDMKVVDDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPFGLYGSKKAGIWSWSHPTAASPRSRPGGACPRGGEPS 359  
Db 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWSWSHPTAASPRSRPGGACPRGGEPS 360  
QY 360 GPRRELKQFLGWLKHKHAYCSNLSFRLYDQWRANMOKSHKTRNDEGILPSGRRGTARGP 419  
Db 361 GPRRELKQFLGWLKHKHAYCSNLSFRLYDQWRANMOKSHKTRNDEGILPSGRRGTARGP 420  
QY 420 AR 421  
Db 421 AR 422  
RESULT 12  
ABU64921  
ID ABU64921 standard; protein; 422 AA.  
AC ABU64921;  
XX  
DT 15-MAY-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO327.  
XX  
KW Human; PRO; secreted protein; transmembrane protein;  
KW Cornelia de Lange syndrome; gene therapy; immune disorder;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;  
KW diabetic complication.  
XX  
OS Homo sapiens.  
XX  
PN US2002173463-A1.  
XX  
PD 21-NOV-2002.  
XX  
PF 31-AUG-2001; 2001US-00944944.  
XX  
PR 03-DEC-1997; 97US-0067411P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 16-DEC-1997; 97US-0069696P.  
PR 16-DEC-1997; 97US-0069702P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 17-DEC-1997; 97US-0069873P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 05-JAN-1998; 98US-0070440P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 01-DEC-1998; 98WO-US025108.  
PR 16-DEC-1998; 98US-0112850P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 28-JUL-1999; 99US-0146222P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.

PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX WPI; 2003-311003/30.  
DR N-PSDB; ABX96790.  
XX  
XX New transmembrane polypeptides and polynucleotides useful for chromosome  
PT identification, tissue typing, gene therapy, in chromosome and gene  
PT mapping, or as molecular weight markers.  
XX  
PS Claim 12; Fig 14; 172pp; English.  
XX  
CC The invention relates to an isolated nucleic acid encoding a secreted/  
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO  
CC polypeptides and their encoding polynucleotides are disclosed. Also  
CC included are a vector comprising the PRO nucleic acid, a host cell  
CC comprising the vector, a process for producing a PRO polypeptide (by  
CC culturing the host cell under conditions for the expression of the PRO  
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an  
CC isolated polypeptide having at least 80% amino acid sequence identity to  
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a  
CC heterologous amino acid sequence and an antibody which specifically binds  
CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,  
CC in chromosome and gene mapping, in generating sense and antisense RNA or  
CC DNA, in generating transgenic or knock-out animals which can be used in  
CC the development and screening of therapeutically useful reagents, and in  
CC gene therapy. The polypeptides may be used as molecular weight markers  
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic  
CC acids may also be used for chromosome identification, and tissue typing.  
CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange  
CC syndrome. Other PRO proteins are variously implicated in immune  
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac  
CC injury, infertility, birth defects, premature aging, cardiac injury,  
CC AIDS, cancer and diabetic complications. The present sequence represents  
CC a PRO protein  
XX  
XX Sequence 422 AA;  
Query Match 99.5%; Score 2279.5; DB 6; Length 422;  
Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 59  
Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60  
QY 60 SVHGDPGATAGLYWTLNGRLPPELSRLVNLASTLALANLNGSRQSGDNLVCHARD 119  
Db 61 SVHGDPGATAGLYWTLNGRLPPELSRLVNLASTLALANLNGSRQSGDNLVCHARD 120  
QY 120 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLYKYLWYQG 179  
Db 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLYKYLWYQG 180  
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLDLVVVTTDPPD 239  
Db 181 DNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLDLVVVTTDPPD 240  
QY 240 VHSVGVGLEDQLSVRWVSPPALKDPLFOAKYQIRYRVSDSVDMKVVDDVSNQTSCLAG 299  
Db 241 VHSVGVGLEDQLSVRWVSPPALKDPLFOAKYQIRYRVSDSVDMKVVDDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPFGLYGSKKAGIWSWSHPTAASPRSRPGGACPRGGEPS 359  
Db 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWSWSHPTAASPRSRPGGACPRGGEPS 360

QY 360 GPVRELKQFLGWLKCHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGTARGP 419  
Db 361 GPVRELKQFLGWLKCHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGTARGP 420  
QY 420 AR 421  
Db 421 AR 422

RESULT 13  
ABUS8355  
ID ABUS8355 standard; protein; 422 AA.  
XX  
AC ABUS8355;  
XX  
14-APR-2003 (first entry)  
XX  
DE Novel human secreted protein PRO327.  
XX  
KW Human; antiinflammatory; antiarteriosclerotic; cardiant; gynecological;  
KW anti-HIV; cytostatic; antidiabetic; BMP-agonist; gene-Therapy;  
KW cytokine-agonist; cytokine-antagonist; gene-Therapy;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defect; premature aging; AIDS; cancer;  
KW diabetic complication.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2002150976-A1.  
XX  
PD 17-OCT-2002.  
XX  
XX 30-AUG-2001; 2001US-00943851.  
XX  
PR 03-DEC-1997; 97US-0067411P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 16-DEC-1997; 97US-0069696P.  
PR 16-DEC-1997; 97US-0069702P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 17-DEC-1997; 97US-0069873P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 05-JAN-1998; 98US-0070440P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 01-DEC-1998; 98WO-US025108.  
PR 16-DEC-1998; 98US-00216021.  
PR 16-DEC-1998; 98US-0112850P.  
PR 22-DEC-1998; 98US-00218517.  
PR 22-DEC-1998; 98US-0113296P.  
PR 03-MAR-1999; 99US-00254311.  
PR 02-JUN-1999; 99WO-US012252.  
PR 28-JUL-1999; 99US-0146222P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX

PA (GETH ) GENENTECH INC.  
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, Kijavini LJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX WPI; 2003-198285/19.  
DR N-PSDB; ABX78444.  
XX  
XX New isolated PRO polypeptide and encoding nucleic acids, useful for the  
PT diagnosis and treatment of disorders such as inflammatory disease,  
PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic  
PT complications.  
XX  
XX Claim 12; Fig 14; 171pp; English.  
XX  
XX The invention describes a novel isolated PRO polypeptide. The methods and  
CC compositions of the present invention are useful for the diagnosis and  
CC treatment of disorders such as inflammatory disease, organ failure,  
CC atherosclerosis, cardiac injury, infertility, birth defects, premature  
CC aging, AIDS, cancer, diabetic complications and mutations in general.  
CC This is the amino acid sequence of a novel human secreted PRO protein  
XX  
XX Sequence 422 AA;  
SQ

Query Match 99.5%; Score 2279.5; DB 6; Length 422;  
Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSAGTAIVISPDPTLLIGSSLLATC 59  
Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSAGTAIVISPDPTLLIGSSLLATC 60  
QY 60 SVHGDPPGATAGLYWTLNGLRPELSRVLNASTLALANLNGSRQSDNLCVCHARD 119  
Db 61 SVHGDPPGATAGLYWTLNGLRPELSRVLNASTLALANLNGSRQSDNLCVCHARD 120  
QY 120 GSILAGSCLYVGLPPEKPNISCKNKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 179  
Db 121 GSILAGSCLYVGLPPEKPNISCKNKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 180  
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDILDVVTDDPPD 239  
Db 181 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDILDVVTDDPPD 240  
QY 240 VHVSRVGGLEDQLSVRWVSPPALKDFLQAKYQIYRVEDSVDMKVDDVSNQTSCLAG 299  
Db 241 VHVSRVGGLEDQLSVRWVSPPALKDFLQAKYQIYRVEDSVDMKVDDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPFYIGSKKAGIWSHWSHPTAASRPRPSPGCGACPRGGEPS 359  
Db 301 LKPGTVYFVQVRCNPFYIGSKKAGIWSHWSHPTAASRPRPSPGCGACPRGGEPS 360  
QY 360 GPVRELKQFLGWLKCHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGTARGP 419  
Db 361 GPVRELKQFLGWLKCHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGTARGP 420  
QY 420 AR 421  
Db 421 AR 422

RESULT 14  
ABUS7241  
ID ABUS7241 standard; protein; 422 AA.  
XX  
AC ABUS7241;  
XX  
DT 04-APR-2003 (first entry)  
XX  
DE Human PRO327 protein.  
XX  
KW Human; antiinflammatory; antiarteriosclerotic; cardiant;

KW anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane;  
 KW anti-inflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility;  
 KW anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect;  
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
 KW premature aging; AIDS; cancer; diabetic complication.

XX Homo sapiens.

XX US2002142958-A1.

XX 03-OCT-2002.

XX 30-AUG-2001; 2001US-00943762.

XX 16-SEP-1998; 98WO-US019330.

XX 01-DEC-1998; 98WO-US025108.

XX 22-JUN-1999; 99WO-US012252.

XX 15-SEP-1999; 99WO-US021090.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 16-DEC-1999; 99WO-US030095.

XX 11-FEB-2000; 2000WO-US003565.

XX 22-FEB-2000; 2000WO-US004414.

XX 02-MAR-2000; 2000WO-US005841.

XX 30-MAR-2000; 2000WO-US008439.

XX 22-MAY-2000; 2000WO-US014042.

XX 28-JUL-2000; 2000WO-US020710.

XX 01-DEC-2000; 2000WO-US032678.

XX 28-FEB-2001; 2001WO-US006520.

XX 25-MAY-2001; 2001US-00866028.

XX (GETH ) GENENTECH INC.

PA Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

XX Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;

PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;

XX N-PSDB; ABX77077.

DR WPI; 2003-174140/17.

XX New secreted and transmembrane nucleic acids and polypeptides, designated

PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,

PT cardiac injury, infertility, birth defects, premature aging, AIDS, or

PT cancer.

XX Claim 1; Fig 14; 173pp; English.

XX This invention relates to a nucleotide sequence encoding an isolated

CC secreted and/or transmembrane protein. The nucleotide sequences of the

CC invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti

CC -infertility, anti-HIV, cytostatic and antidiabetic activities and may be

used in gene therapy. The nucleic acids and polypeptides are useful for  
 CC treating inflammatory diseases, organ failure, atherosclerosis, cardiac  
 CC injury, infertility, birth defects, premature aging, AIDS, cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing. The present  
 CC sequence represents a protein encoded by the nucleic acids of the  
 CC invention

XX Sequence 422 AA;

SQ

Query Match 99.5%; Score 2279.5; DB 6; Length 422;

Best Local Similarity 99.8%; Pred. No. 3.9e-184;

Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 MPAGRGPAAQARRPPPLP-ILLCLVLGAPRAGSANTAVISPODPTLLIGSSLLATC 59

1 MPAGRGPAAQARRPPPLP-ILLCLVLGAPRAGSANTAVISPODPTLLIGSSLLATC 60

60 SVHGDPPGATAGLYWTNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 119

Db 61 SVHGDPPGATAGLYWTNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 120  
 QY 120 GSILAGSCLYVGLPPEKPNVSCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQG 179  
 Db 121 GSILAGSCLYVGLPPEKPNVSCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQG 180  
 QY 180 DNTCEYHTVGHPSCHIPKDLALFPTPEIWEATNRLGARSDDLTLDLVVTDDPPD 239  
 Db 181 DNTCEYHTVGHPSCHIPKDLALFPTPEIWEATNRLGARSDDLTLDLVVTDDPPD 240  
 QY 240 VHSVSVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLLAG 299  
 Db 241 VHSVSVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLLAG 300  
 QY 300 LKPGTVYFVQVRCNPFYGVSKKAGIWEWSHPTAASPRSRPFGGGACPRGGEPS 359  
 Db 301 LKPGTVYFVQVRCNPFYGVSKKAGIWEWSHPTAASPRSRPFGGGACPRGGEPS 360  
 QY 360 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNDEGILPSGRGTARGP 419  
 Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNDEGILPSGRGTARGP 420  
 QY 420 AR 421  
 Db 421 AR 422

RESULT 15

ABUS6306

ID ABUS6306 standard; protein; 422 AA.

XX AC ABUS6306;

XX DT 31-MAR-2003 (first entry)

XX DE Human secreted/transmembrane protein, PRO327.

XX KW Human; PRO; antiinflammatory; antiarteriosclerotic; cardiant;

XX KW gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease;

XX KW organ failure; atherosclerosis; cardiac injury; infertility;

XX KW birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;

XX KW cancer; diabetic complication.

XX OS Homo sapiens.

XX PN US2002132981-A1.

XX PD 19-SEP-2002.

XX PF 30-AUG-2001; 2001US-00944396.

XX PP 03-DEC-1997; 97US-0067411P.

PR 11-DEC-1997; 97US-0069278P.

PR 11-DEC-1997; 97US-0069334P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 16-DEC-1997; 97US-0069694P.

PR 16-DEC-1997; 97US-0069696P.

PR 17-DEC-1997; 97US-0069702P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0069873P.

PR 18-DEC-1997; 97US-0068017P.

PR 05-JAN-1998; 98US-0070440P.

PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.

PR 25-FEB-1998; 98US-0075945P.

PR 16-SEP-1998; 98WO-US019330.

PR 01-DEC-1998; 98WO-US025108.

PR 16-DEC-1998; 98US-0112850P.

PR 22-DEC-1998; 98US-0113296P.

PR 02-JUN-1999; 99WO-US012252.

PR 28-JUL-1999; 99US-0146222P.

PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 25-MAY-2001; 2001US-00866028.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;  
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;  
PI Hillan KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;  
XX  
DR WPI; 2003-147446/14.  
DR N-PSDB; ABX75909.  
XX  
XX New isolated PRO polypeptide and encoding nucleic acids, useful for the  
PT diagnosis and treatment of disorders such as inflammatory disease,  
PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic  
PT complications.  
XX  
PS Claim 12; Fig 14; 171pp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide having at least 80%  
CC amino acid sequence identity to and scoring at least 80% positives when  
CC compared to any of 15 fully defined sequences of 235-954 amino acids,  
CC given in the specification. Also included are: (1) an isolated PRO  
CC nucleic acid having at least 80% nucleic acid sequence identity to a  
CC nucleotide sequence that encodes PRO or its extracellular domain, and  
CC comprising any of 15 fully defined nucleotide sequences of 957-3441 bp,  
CC given in the specification and deposited under ATCC accession number  
CC 209526, 209508, 209528, 209530, 209523, 209492, 209532, 209531,  
CC 209529, 209527, 209570, 209618, 209621 and 209619; (2) a vector  
CC comprising the PRO nucleic acid; (3) a host cell comprising the vector;  
CC (4) producing PRO polypeptides, comprising culturing the cell for  
CC expression of the PRO polypeptide and recovering the PRO polypeptide from  
CC the cell culture; (5) a chimaeric molecule comprising PRO fused to a  
CC heterologous amino acid sequence; and (6) an anti-PRP antibody. The  
CC methods and compositions are useful for the diagnosis and treatment of  
CC disorders such as inflammatory disease, organ failure, atherosclerosis,  
CC cardiac injury, infertility, birth defects, premature aging, AIDS  
CC (acquired immunodeficiency syndrome), cancer, diabetic complications and  
CC mutations in general. The present sequence is a PRO polypeptide  
XX  
XX Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;  
Best Local Similarity 99.8%; Pred. No. 3.9e-184;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGGAHTAVISPDPTLLIGSSLLATC 59  
DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGGAHTAVISPDPTLLIGSSLLATC 60  
QY 60 SVHGDPGATAGLWTLNGLRLPPELSRVLNASTLALANLNGSRSGDNLVCHARD 119  
DB 61 SVHGDPGATAGLWTLNGLRLPPELSRVLNASTLALANLNGSRSGDNLVCHARD 120  
QY 120 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAGHGTFLHTNYSKYLKRWYQG 179  
DB 121 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAGHGTFLHTNYSKYLKRWYQG 180  
QY 180 DNTCEYHTVGHSHCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDLWVTTDPPPD 239  
DB 181 DNTCEYHTVGHSHCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDLWVTTDPPPD 240

Search completed: April 11, 2006, 02:09:57  
Job time : 116.031 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 02:10:19 ; Search time 21.0667 Seconds  
(without alignments)  
1922.808 Million cell updates/sec

Title: US-09-037-657-44  
Perfect score: 2290  
Sequence: 1 MPAGRRGPAQSAQRRPPLL.....NQDEILPSRRGTARGPAR 421

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	14.5	288	B59405	prolactin receptor
2	332	14.5	376	A59405	prolactin receptor
3	332	14.5	622	A40144	prolactin receptor
4	323	14.1	918	A36337	membrane glycoprot
5	317.5	13.9	917	I49699	glycoprotein 130 -
6	316	13.8	830	I50455	prolactin receptor
7	314.5	13.7	918	A44257	interleukin-6 sign
8	313	13.7	310	A29884	prolactin receptor
9	313	13.7	412	A41070	prolactin receptor
10	313	13.7	610	A34631	prolactin receptor
11	313	13.7	610	A36116	prolactin receptor
12	309.5	13.5	292	I77524	prolactin receptor
13	309.5	13.5	303	I77524	prolactin receptor
14	309.5	13.5	608	I53269	prolactin receptor
15	308	13.4	831	QJ1655	prolactin receptor
16	306.5	13.4	581	I45971	prolactin receptor
17	300.5	13.1	616	A30304	prolactin receptor
18	263.5	11.5	630	I51086	prolactin receptor
19	255.5	11.2	837	A34898	granulocyte colony
20	249	10.9	372	I58141	ciliary neurotroph
21	242.5	10.6	771	B38252	granulocyte colony
22	242.5	10.6	783	JH0329	granulocyte colony
23	242.5	10.6	863	C38252	granulocyte colony
24	236	10.3	372	UHHUCN	ciliary neurotroph
25	211.5	9.2	362	S60614	growth promoting a
26	211.5	9.2	422	I37891	interleukin-11 rec
27	208.5	9.1	432	I48343	interleukin-11 rec
28	201	8.8	468	A41242	interleukin-6 rece
29	200	8.7	1097	S17308	leukemia inhibitor

30	199.5	8.7	460	2	JL0145	interleukin-6 rece
31	199	8.7	156	2	A32868	prolactin receptor
32	194.5	8.5	805	2	S68441	leptin receptor, s
33	194.5	8.5	892	2	S68439	leptin receptor, s
34	194.5	8.5	894	2	S68437	leptin receptor, s
35	194.5	8.5	900	2	S68440	leptin receptor, s
36	194.5	8.5	1162	2	S68438	leptin receptor, s
37	194	8.5	625	2	S35317	hematopoietic grow
38	191.5	8.4	440	2	JL0144	interleukin-6 rece
39	191	8.3	150	2	B34631	lactogen receptor
40	190.5	8.3	1162	2	PC4184	leptin receptor, O
41	190	8.3	626	2	S37622	proto-oncogene - m
42	187	8.2	1092	2	JK0312	differentiation-ac
43	186.5	8.1	579	2	B45266	MPL-K protein prec
44	186.5	8.1	635	2	A45266	MPL-P protein prec
45	184	8.0	895	2	S74225	leptin receptor, i

ALIGNMENTS

RESULT 1

B59405

prolactin receptor short form Sib precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence revision 01-Feb-2002 #text\_change 09-Jul-2004

C:Accession: B59405; B49400

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin recep

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: B59405

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU>

A:Cross-references: UNIPROT:Q96P36; UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1

R:Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: B49400

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU2>

A:Cross-references: UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1

C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor ,

ta-casain gene promoter activation, with S1b more effective than S1a. However, their li

C:Genetics: GDB:PRLR

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-288/Product: prolactin receptor, short form Sib #status predicted <MAY>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59.104,233/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 14.5%; Score 332; DB 2; Length 288;

Best Local Similarity 37.1%; Pred No. 1.7e-18;

Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY	122	ILAGSCLVYG-LPPKPKVNI	SCSKMKDLTCRWTFGAHGETFLHNTYSLKYLRYGQD	180
Db	15	LFPLNTCLLNGQLPPCKP	EIFKCRSPNKETFTCWRRFGTDGG--LPNTYSLTYHREGETLM	72
QY	181	NTCEBYHTVGHPSCHIP	KD-LALFPTYEIWVETARLGSARSDVLTLDLDVVTDPDPPD	239
Db	73	HECPDYITGGPNSCHFG	KYQYTSMMWTYIMMVNATNMGSPFSDLYVDVYTYVQDPDPLE	132
QY	240	VHVSRRVGGLEDQLSV	RVWV--SPALKDF--LFOAKYQIRYRVSDVDMKWVDDVSNQTS	294
Db	133	LAV-EVKQPEDRKPYL	WIKWSPPTLIDLKTGHTFTLLYELRLKPKAAEWE-IHFAGQQTTE	190
QY	295	CRLAGLKPGTVYFVQV	RNCNPFGIYGGKKAGIWSNSHPTAASTP	338



```
Db 91 FTDIASLNTQLTCNLTITGQLBQNVYGITIIISGLPEKPKNLSCVINEGKQKRCWDGGR 150
Qy 159 HGETFLHTNYSKYLKRWYQDNTCEVEYHTVGPSPHSCHIPKDLALFTPYEIVWEATNRLGS 218
Db 151 --ETHLETNFTLKSEWATHKPADCKAKRT--PTSCVTVDYSIVYFVNIWVWEAENALOK 206
Qy 219 ARSDVLTDLILDVTTDPPDVHVRVSGGLEQLSVRVVSPPALKDFLFOAKYQIRYRVE 278
Db 207 VTSDFHINFDVYKVPNPPHNLVINSEBELSLTLKLTWN-PSIKSVII-LKYNIQYRTK 264
Qy 279 DSDVWKV---DDVSNQTSCLAGKPGYVYFVQVRCNPPFGIYGSKKAGIWSHSPRAA 335
Db 265 DASTWSQIPPEPTASTRSFTVQDLKPFTYVFRIRC-----MKEDGKGYSWDSERASG 319
Qy 336 STPRSERP 343
Db 320 IT-YEDRP 326

RESULT 5
I49699
Glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:192291532; PMID:1602143
A:Accession: I49699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPROT:Q00560; UNIPARC:UPI000002845A; GB:M83336; NID:G193591; PIDN:
F:134-314/Domain: cytokine receptor homology <CRS>
A:Accession: I48370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RE2>
A:Cross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:G840816; PIDN:CAA44515.1; PI
C:Genetics:
A:Gene: gp130
A:Interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.B.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257; MUID:93052397; PMID:1427893
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 317.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 9.7e-17;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

Qy 42 ISPDPTLLIGSSLLATCSVHG---DPPGATAEGLYWTNGRRRLPELSRVLNASTLALA 98
Db 31 IYPEFPVQVQSGNFTACVLEKACIQHYVYNASIVWKTNHAAPREQVTVINRTTSVT 90
Qy 99 LANLNGSRQRSGDNLVCHARDGSLIAGSCLYVGLPEKPKVNSCSWKMDLTCRWTPCA 158
Db 91 FTDVVLPSVQLTCNILLSFGQIEQNVGVVTMLGFFPDKPTNLTCVINEGKMLCQWDGFR 150
Qy 159 HGETFLHTNYSKYLKRWYQD-NTCEEYHTVGPSPHSCHIPKDLALFTPYEIVWEATNRLG 217
Db 151 --ETYLETNYTLKSE--WATEKFPQCQSKHGT---SCWVSVMPTTYVNIWVWEAENALG 203
Qy 218 SARSDVLTDLILDVTTDPPDVHVRVSGGLEQLSVRVVSPPALKDFLFOAKYQIRYRV 277
Db 204 KYSSININFDVYKVPNPPHNLVINSEBELSLKLSWSSGL--GGLLDKSLDIQVRT 261
Qy 278 EDSVDWKV---DDVSNQTSCLAGKPGYVYFVQVRCNPPFGIYGSKKAGIWSHSPTA 334
Db 262 KDASTWIQVPLEDTWSPTSFTVQDLKPFTYVFRIR----SIKDSGK-GYWSDSERAS 316
Qy 335 AST--PRSERP 343
Db 317 GTTYEDRPSPR 327
```

## RESULT 6

```
I50455
Prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267; PMID:7516866
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHS>
A:Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:G466381; PI
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 13.8%; Score 316; DB 2; Length 830;
Best Local Similarity 36.6%; Pred. No. 1.1e-16;
Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps 8;

Qy 133 PPEKPVNISCWKMKDLTCRWTPGAHGETFLH-TNYSIKYLKRWYQDNTCEEYHTVGP 191
Db 231 PPEKPTIIKCRSPEKETFTCWMPGSDG--HPTNVTLLYSKEGEERVYECPDYKTAGP 287
Qy 192 HSCHI-PKDLALFTPYEIVWEATNELGARSQVLTLDILDVTTDPPDV--HVSRVGGL 248
Db 288 NSCYFDKXHTSFWTIYNTVTKATNIGSNVSDPLVYDVTYIVQTPPPVNVNLTLEKKTVNR 347
Qy 249 EDQLSVRVVSPPALKDF---LFQAKYQIRYRVSDVMDKVDVSDVSNQTSCLAGLKPQTV 305
Db 348 KPYLVLTW-SPPLADVRSGLTLDLYELRLKPEBAEWETI-FVQQTHYKMFSLNPGKK 405
Qy 306 YFVQVRCNPPFGIYGSKKAGIWSWS 330
Db 406 YIVQIHCKP-----DHHGWSWSWS 424

RESULT 7
A44257
Interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.B.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257; MUID:93052397; PMID:1427893
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 314.5; DB 2; Length 918;
Best Local Similarity 29.7%; Pred. No. 1.7e-16;
Matches 93; Conservative 51; Mismatches 140; Indels 29; Gaps 11;

Qy 42 ISPDPTLLIGSSLLATC-----SVHGDPPGATAEGLYWTNGRRRLPELSRVLNAST 94
Db 31 IYPEFPVQVQSGNFTATCVLEKCLQVY---SVNATYIVWKTNHAAPREQVTVINRTA 86
Qy 95 LALANLNGSRQRSGDNLVCHARDGSLIAGSCLYVGLPEKPKVNSCSWKMDLTCRW 154
Db 87 SSVTFDVFVQNVQVLTCTNLSFGQIEQNVYGITILSGYPPDIPTNLSCLVINEGKMLCOL 146
Qy 155 TPGAHGETFLHTNYSKYLKRWYQD-NTCEEYHTVGPSPHSCHIPKDLALFTPYEIVWEAT 213
```

Db 147 DGR--EYLENYILKSE--WATEKFPDCRTH--GTSSCMGYTPYFVNIEVVAE 200  
QY 214 NRLGARSVDLFDILDVTTDPPDPVHVSRYGGLDQLSVRWSPALKDPLFOAKYQI 273  
Db 201 NALGNVSSPINFDPVKPSPHNLSVTNSEELSSILKLAWNSGL--DSILRLKSDI 258  
QY 274 RYRVSDVDWKV---DDVSNOTSRLAGLKGTYVFQVRCNPGIYGSKKAGIWSWS 330  
Db 259 QYRTKDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIR----SIXENGR-GYWSOWS 313  
QY 331 HPTAASTPRSERP 343  
Db 314 E-EASGTYYEDRP 325  
RESULT 8  
A29884  
prolactin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C:Accession: A29884  
R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shiota, M.; Banville  
Cell 53, 69-77, 1988  
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho  
A:Reference number: A29884; MUID:88165059; PMID:2832068  
A:Accession: A29884  
A:Molecule type: mRNA  
A:Residues: 1-310 <BOU>  
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:  
A:Keywords: transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-310/Product: prolactin receptor #status predicted <MAT>  
F:31-216/Domain: cytokine receptor homology <CRS>  
Query Match 13.7%; Score 313; DB 2; Length 310;  
Best Local Similarity 35.0%; Pred. No. 5.7e-17;  
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;  
QY 121 SILAGSCLYVGLPPEKPNVNIWSCNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYGD 180  
Db 15 SLKKGQS-----PPGKPEIHKCRSPDKETFTCWNPNGTDGG--LPNYSLSYSKE--GEK 65  
QY 181 NT--CEEYHTVGHSPHCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPP 237  
Db 66 TTVECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTYIIVEPEPP 125  
QY 238 PDVHVSRYGGLDQLSVRWV--SPPALKDF---LFQAKYQIRYRVSDVDWKVDDVSNQ 292  
Db 126 RNLTLL-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPEAEWE--IHFTGHQ 183  
QY 293 TSCRLAGLPGTYVFQVRCNPGIYGSKKAGIWSWSHPTAATP 338  
Db 184 TQKVPFDLYPGQKYLVTQCKP-----DHGYNSRWSQESSVEMP 222  
RESULT 9  
A41070  
prolactin receptor Nb2 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: A41070; I55417  
R:Ali, S.; Pellegrini, I.; Kelly, P.A.  
J. Biol. Chem. 266, 20110-20117, 1991  
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolact  
A:Reference number: A41070; MUID:92041834; PMID:1718958  
A:Accession: A41070  
A:Molecule type: mRNA  
A:Residues: 1-412 <ALI>  
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:  
R:O'Neal, K.D.; Yu-Lee, L.Y.  
J. Biol. Chem. 269, 26076-26082, 1994  
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor

A:Reference number: I55417; MUID:95014432; PMID:7929319  
A:Accession: I55417  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-412 <RES>  
A:Cross-references: UNIPARC:UPI000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PI  
A:Experimental source: Nb2-11C cell line  
C:Keywords: transmembrane protein  
F:31-216/Domain: cytokine receptor homology <CRS>  
Query Match 13.7%; Score 313; DB 2; Length 412;  
Best Local Similarity 35.0%; Pred. No. 8.1e-17;  
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;  
QY 121 SILAGSCLYVGLPPEKPNVNIWSCNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYGD 180  
Db 15 SLKKGQS-----PPGKPEIHKCRSPDKETFTCWNPNGTDGG--LPNYSLSYSKE--GEK 65  
QY 181 NT--CEEYHTVGHSPHCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPP 237  
Db 66 TTVECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTYIIVEPEPP 125  
QY 238 PDVHVSRYGGLDQLSVRWV--SPPALKDF---LFQAKYQIRYRVSDVDWKVDDVSNQ 292  
Db 126 RNLTLL-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPEAEWE--IHFTGHQ 183  
QY 293 TSCRLAGLPGTYVFQVRCNPGIYGSKKAGIWSWSHPTAATP 338  
Db 184 TQKVPFDLYPGQKYLVTQCKP-----DHGYNSRWSQESSVEMP 222  
RESULT 10  
A34631  
lactogen receptor 1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 13-Jul-1990 #sequence\_revision 09-Oct-1992 #text\_change 09-Jul-2004  
C:Accession: A34631  
R:Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.  
Biochem. Biophys. Res. Commun. 168, 415-422, 1990  
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA  
A:Reference number: A34631; MUID:90241201; PMID:2159291  
A:Accession: A34631  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-610 <ZHA>  
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170BE1; GB:M34083; NID:g205122; PIDN  
A>Note: the authors translated the codon GAG for residue 533 as Gly  
F:31-216/Domain: cytokine receptor homology <CRS>  
Query Match 13.7%; Score 313; DB 2; Length 610;  
Best Local Similarity 35.0%; Pred. No. 1.3e-16;  
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;  
QY 121 SILAGSCLYVGLPPEKPNVNIWSCNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYGD 180  
Db 15 SLKKGQS-----PPGKPEIHKCRSPDKETFTCWNPNGTDGG--LPNYSLSYSKE--GEK 65  
QY 181 NT--CEEYHTVGHSPHCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPP 237  
Db 66 TTVECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTYIIVEPEPP 125  
QY 238 PDVHVSRYGGLDQLSVRWV--SPPALKDF---LFQAKYQIRYRVSDVDWKVDDVSNQ 292  
Db 126 RNLTLL-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPEAEWE--IHFTGHQ 183  
QY 293 TSCRLAGLPGTYVFQVRCNPGIYGSKKAGIWSWSHPTAATP 338  
Db 184 TQKVPFDLYPGQKYLVTQCKP-----DHGYNSRWSQESSVEMP 222  
RESULT 11  
A36116  
prolactin receptor 2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: A36116  
R:Shioto, M.; Banville, D.; Ali, S.; Jolicœur, C.; Boutin, J.M.; Edery, M.; Djiane, J.  
Mol. Endocrinol. 4, 1136-1143, 1990  
A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.  
A:Reference number: A36116; MUID:91155946; PMID:2293022  
A:Accession: A36116  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-610 <SHI>  
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170ADB; GB:M57668; NID:g206366; PIDN:  
P:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 313; DB 2; Length 610;  
Best Local Similarity 35.0%; Pred. No. 1.3e-16;  
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

QY 121 SLLAGSLVGLPPEKPNVISCWKNKDLTCWTGAGHETFLHTNYSKYKLRWYQD 180  
DB 15 SLLKGSQ-----PPGKPEIHKCRSPDKETFTCMWNGFTDGG--LPTNYSLTYSKE--GEK 65

QY 181 NT--CEYHTVGHPSCHIPKD-LALFPTPEIWEATNRLGARSVDLTLDLDVTTDPP 237  
DB 66 TTYECPDYKTSKPNSCFFSKQYTSIWKIYIITVATNMGSSSDPLYVDVTIYVEPEPP 125

QY 238 PDVHVSRLGLEDQLSVRWV--SPPALKDF---LFOAKYQIRYRVSDVDKVVDDVSNQ 292  
DB 126 RNLT-L-EVKQLDKKTYLWVKSPPITDVKTGFTMEYERLKPGEAEWE-IHFTGHQ 183

QY 293 TSCRLAGLPGTYVFVQVRCNPGIYGSKAGIWSHPTAASP 338  
DB 184 TQFKVFDLYPGQKYLVTQTRCKP-----DHGYMSRWSSQESSVEMP 222

RESULT 12  
I77525  
prolactin receptor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I77525  
R:Davis, J.A.; Linzer, D.I.H.  
Mol. Endocrinol. 3, 674-680, 1989  
A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
A:Reference number: I57699; MUID:89261824; PMID:2725531  
A:Accession: I77525  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-292 <RES>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B198; GB:M22959; NID:g200481; PIDN:  
P:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 309.5; DB 2; Length 292;  
Best Local Similarity 31.4%; Pred. No. 9.9e-17;  
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 86 LSRVLNASTLALANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPNVISCWSK 145  
DB 1 MSSALAYMLLVLSILNQSQ-----PPGKPEIHKCRSP 34

QY 146 NMKDLTCRWTPGAGHETFLHTNYSKYKLRWYQDNT--CEYHTVGHPSCHIPKD-LAL 202  
DB 35 DKETFTCMWNGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSKPNSCFFSKQYTSI 90

QY 203 FPTYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSRLGLEDQLSVRWVS--PP 260  
DB 91 WKIYIITVATNMGSSSDPLYVDVTIYVEPEPRNLTL-EVKQLDKKTYLWVKWLP 149

RESULT 14  
I53269  
prolactin receptor, long form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I53269; JT0671; S34356  
R:Clarke, D.B.; Linzer, D.I.H.  
Endocrinology 133, 224-232, 1993  
A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.  
A:Reference number: I53269; MUID:93307149; PMID:8319571  
A:Accession: I53269  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-608 <RES>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:L14811; NID:g293769; PIDN:  
R:Moore, R.C.; Oka, T.  
Gene 134, 263-265, 1993  
A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form  
A:Reference number: JT0671; MUID:94085788; PMID:8262385  
A:Accession: JT0671  
A:Molecule type: mRNA  
A:Residues: 1-608 <MOO>  
A:Cross-references: UNIPARC:UPI0000020E90; GB:L13593; NID:g347398; PIDN:AAC37641.1; PID  
R:Edery, M.; Peret, A.; Nandi, S.; Kelly, P.A.  
submitted to the EMBL Data Library, June 1993  
A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.  
A:Reference number: S34356

DB 206 ----DHGYMSRWGQEKSIPI 222

RESULT 13  
I77524  
prolactin receptor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I77524  
R:Davis, J.A.; Linzer, D.I.H.  
Mol. Endocrinol. 3, 674-680, 1989  
A:Title: Expression of multiple forms of the prolactin receptor in mouse liver.  
A:Reference number: I57699; MUID:89261824; PMID:2725531  
A:Accession: I77524  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-303 <RES>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B197; GB:M22958; NID:g200479; PIDN:  
P:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 309.5; DB 2; Length 303;  
Best Local Similarity 31.4%; Pred. No. 1e-16;  
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 86 LSRVLNASTLALANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPNVISCWSK 145  
DB 1 MSSALAYMLLVLSILNQSQ-----PPGKPEIHKCRSP 34

QY 146 NMKDLTCRWTPGAGHETFLHTNYSKYKLRWYQDNT--CEYHTVGHPSCHIPKD-LAL 202  
DB 35 DKETFTCMWNGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSKPNSCFFSKQYTSI 90

QY 203 FPTYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSRLGLEDQLSVRWVS--PP 260  
DB 91 WKIYIITVATNMGSSSDPLYVDVTIYVEPEPRNLTL-EVKQLDKKTYLWVKWLP 149

QY 261 ALKDF---LFOAKYQIRYRVSDVDKVVDDVSNQTSCLAGLPGTYVFVQVRCNPFPI 317  
DB 150 TITDVKTGFTMEYERLKSBEADWE-IHFTGHQTFQKVFYDLYPGQKYLVTQTRCKP--- 205

QY 318 YGSKKAGIWSHPTAASP 338

DB 206 ----DHGYMSRWGQEKSIPI 222

RESULT 14  
I53269  
prolactin receptor, long form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I53269; JT0671; S34356  
R:Clarke, D.B.; Linzer, D.I.H.  
Endocrinology 133, 224-232, 1993  
A:Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.  
A:Reference number: I53269; MUID:93307149; PMID:8319571  
A:Accession: I53269  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-608 <RES>  
A:Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:L14811; NID:g293769; PIDN:  
R:Moore, R.C.; Oka, T.  
Gene 134, 263-265, 1993  
A:Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form  
A:Reference number: JT0671; MUID:94085788; PMID:8262385  
A:Accession: JT0671  
A:Molecule type: mRNA  
A:Residues: 1-608 <MOO>  
A:Cross-references: UNIPARC:UPI0000020E90; GB:L13593; NID:g347398; PIDN:AAC37641.1; PID  
R:Edery, M.; Peret, A.; Nandi, S.; Kelly, P.A.  
submitted to the EMBL Data Library, June 1993  
A:Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.  
A:Reference number: S34356

```

Qy      306 YFVQVRCNPFGLYGSKKAGIWSHPTAAASTPRSR 342
      : : : : :
      : : : : :
Db      405 YIIQTHCKP-----DHHGSHSENSNYIQIPNDFR 435

Search completed: April 11, 2006, 02:17:27
Job time : 22.0667 secs

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A:Accession: S34356
A:Molecule type: mRNA
A:Residues: 1-557, 'F', 559-608 <DE>
A:Cross-references: UNIPARC:UPI0000163B24; EMBL:X73372; NID:G312696; PIDN:CAA51789.1; PI
C:Comment: Prolactin receptor have long form and short form which are resulted from alte
C:Comment: This long form receptor is capable of transducing a signal to milk protein ge
C:Keywords: receptor; transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>
F:230-253/Domain: transmembrane #status predicted <TM>

Query Match      13.5%; Score 309.5; DB 2; Length 608;
Best Local Similarity 31.4%; Pred. No. 2.5e-16;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

Qy      86 LSRVLNASTLALANLINGSRQSRGDNLVCHARDGSLAGSLCYLVGLPPEKPVNISCWSK 145
Db      1 MSSALAYMLLVLSISLNGQS-----PPGKEPIHCKRSP 34

Qy      146 NKKDLTCRWTPCAHGTEFTLHTNYSLVKLRYWGQDNT--CBEYHTVGPHSCHIPKD-LAL 202
Db      35 DKETTCWNPQSDGG--LPTNYSLYSKY-GEKNYECPDYKTSGPSNCSFFSKQYTSI 90

Qy      203 FTFPIYIWEATNRLGSGARDSVLTLDILDVVTTPPPDHVSRYVGGLEDQLSVRWVS---PP 260
Db      91 WKIYIITVNATNMGSGSTSDPLYVDVTYIIVEPSPRNLTL-EVKQLDKKTYLWVKWLP 149

Qy      261 ALKDF---LFOAKYQIYRYVEDSVDMKVDVDSNQTSCRLAGLKPQTVYFQVRCNPFGI 317
Db      150 TITDVKTGHTWEYERILKSEADEWE-IHFTGHQTFQKVPFDLYPGQKYLVTQCKP--- 205

Qy      318 YGSKKAGIYSEWSHPTAASTP 338
Db      206 ----DHGYWSRWGOEKSIEIP 222

```

RESULT 15  
JQ1655  
prolactin receptor precursor - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: JQ1655  
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.  
Biochem. Biophys. Res. Commun. 188, 490-496, 1992  
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se  
A:Reference number: JQ1655; MUID:93075121; PMID:1445292  
A:Accession: JQ1655  
A:Molecule type: mRNA  
A:Residues: 1-831 <YAN>  
A:Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DDBJ:D13154; NID:G222848; PID  
A:Experimental source: kidney  
A:Keywords: glycoprotein; transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-831/Product: prolactin receptor #status predicted <MAT>  
F:36-219/Domain: cytokine receptor homology <CRS1>  
F:233-425/Domain: cytokine receptor homology <CRS2>  
F:439-462/Domain: transmembrane #status predicted <TM>  
F:59.91/Domain: 100.112.132.262.303.315.335.647.701.800/Binding site: carbohydrate (Asn) (coval

	Query Match	13.4%	Score 308;	DB 2;	Length 831;
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				Indels	18; Gaps
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Db	230	PPEKPTIIRKCRSPKETFTTCWPKGLDGG---HPTNYTLKYSKEGEEQVYECPDRTATGP	286		
Qy	192	HSCHI-PKDLALTPPEIWEATNRGLSARDVLTLDILDVVTTPPPDV--HVSVRVGL	248		
Db	287	NSCYFDKKTSHFTIINITVRATNEMGSNSSDPHVDVTYIVQDPFPVNVLTLELKKPINR	346		
Qy	249	EDQLSVRVWSPPALKDF---LFQAKYQIRYRVSDSVDMKWVDDVSNQTSRLAGLKPQTV	305		
Db	347	KPYLVLTW-SPPPLADYRSGLWLTLEYELRLKPEEGEEWETI-FVCGQOTQYKMFSLNPQKK	404		

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:04:23 ; Search time 125.397 Seconds  
(without alignments)  
2368.694 Million cells updates/sec

Title: US-09-037-657-44  
Perfect score: 2290  
Sequence: 1 MPAGRRGPAQAQARRPPPL.....NODEGILSGRRGTARGPAR 421

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2279.5	99.5	422	1 CRLF1_HUMAN	Q75462 homo sapien
2	2178	95.1	425	1 CRLF1_MOUSE	O91m58 mus musculu
3	1418.5	61.9	389	2 O6DG28_BRARE	Q69g28 brachydanio
4	1384.5	60.5	394	2 O6UAQ5_TETNG	O6uaq5 tetraodon n
5	994	43.4	437	2 Q4RMP5_TETNG	Q4rmp5 tetraodon n
6	466.5	20.4	207	2 Q4TCM7_TETNG	Q4tcm7 tetraodon n
7	406	17.7	151	2 Q4RDR1_TETNG	Q4rdr1 tetraodon n
8	380	16.6	199	2 Q4RDQ9_TETNG	Q4rdq9 tetraodon n
9	365.5	16.0	918	2 Q9W6U9_CHICK	Q9w6u9 gallus gall
10	354	15.5	881	2 O57519_XENLA	O57519 xenopus lae
11	333	14.5	268	2 Q8TD78_HUMAN	Q8td78 homo sapien
12	332	14.5	288	2 Q9GP36_HUMAN	Q9gp36 homo sapien
13	332	14.5	349	2 Q9UHQ5_TETNG	Q9uhj5 homo sapien
14	332	14.5	376	2 Q9GP35_HUMAN	Q9gp35 homo sapien
15	332	14.5	622	2 PRLR_HUMAN	P16471 homo sapien
16	332	14.5	622	2 O5EAW0_PONPY	O5raw0 pongo pygma
17	327.5	14.3	1010	2 Q7TQ89_RAT	Q7tcq9 rattus norv
18	323	14.1	857	2 Q9FC04_HUMAN	Q5fc04 homo sapien
19	323	14.1	918	1 IL6RB_HUMAN	P40189 homo sapien
20	317.5	13.9	917	1 IL6RB_MOUSE	Q00560 mus musculu
21	317.5	13.9	917	2 Q6PD15_MOUSE	Q6pd19 mus musculu
22	317	13.8	622	2 Q9N0J7_CALJA	Q9n0j7 callithrix
23	316	13.8	830	1 PRLR_COLLI	Q90374 columbia liv
24	315	13.8	622	2 Q8E5V4_CEBAP	Q8e5v4 cebus apell
25	314.5	13.7	918	1 IL6RB_RAT	P40190 rattus norv
26	313	13.7	310	2 Q58DZ7_RAT	Q58dz7 rattus norv
27	313	13.7	610	1 PRLR_RAT	P05710 rattus norv
28	309.5	13.5	292	2 Q8C7G1_MOUSE	Q8c7g1 mus musculu
29	309.5	13.5	581	1 PRLR_SHEEP	Q46561 ovis aries
30	309.5	13.5	608	1 PRLR_MOUSE	Q08501 mus musculu
31	309.5	13.5	608	2 Q99JZ1_MOUSE	Q99jz1 mus musculu

32	308	13.4	460	2 Q7T220_CHICK	Q7t220 gallus gall
33	308	13.4	625	1 PRLR_PIG	Q6jta8 sus scrofa
34	308	13.4	831	1 PRLR_CHICK	Q04594 gallus gall
35	308	13.4	831	2 Q6QDA0_CHICK	Q6qda0 gallus gall
36	307	13.4	831	1 PRLR_MELGA	Q21094 meleagris g
37	306.5	13.4	581	1 PRLR_BOVIN	Q28172 bos taurus
38	304	13.3	581	1 PRLR_CEREL	Q28235 cervus elap
39	300.5	13.1	616	1 PRLR_RABIT	P14787 oryctolagus
40	294	12.8	611	2 Q9PTH9_XENLA	Q9pth9 xenopus lae
41	292.5	12.8	611	2 Q9TBF6_XENLA	Q9tbf6 xenopus lae
42	292.5	12.8	611	2 Q9PTI0_XENLA	Q9pti0 xenopus lae
43	291.5	12.7	604	2 Q6UAP8_TETNG	Q6uap8 tetraodon n
44	291	12.7	357	2 Q4SQD8_TETNG	Q4sqd8 tetraodon n
45	291	12.7	870	2 Q6UAN0_TETNG	Q6uan0 tetraodon n

ALIGNMENTS

RESULT 1  
CRLF1\_HUMAN STANDARD; PRT; 422 AA.  
AC O75462; Q9UHQ5;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)  
DE (CLF-1) (CYTOR5).  
GN Name=CRLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1] NUCLEOTIDE SEQUENCE, SUBUNIT, SUBCELLULAR LOCATION, TISSUE  
RP SPECIFICITY, AND INDUCTION.  
RX MEDLINE=98349389; PubMed=9686600;  
RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,  
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;  
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with  
members of the cytokine type I receptor family.";  
J. Immunol. 161:1371-1379(1998).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RA Magrangeas F., Jacques Y., Minvielle S.;  
RT "Cloning and expression of a novel soluble protein containing  
hematopoietic cytokine receptor domains.";  
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RA Lok S., Presnell S.R., Jernberg A.C., Gilbert T., Whitmore T.E.,  
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;  
RN Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
[4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RA MEDLINE=28887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,  
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
RA Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment.";  
Genome Res. 13:2265-2270(2003).  
[5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

CC RX TISSUE=Lymph;  
 CC RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 CC RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 CC RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 CC RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 CC RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 CC RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 CC RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 CC RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 CC RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 CC RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 CC RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;  
 CC RT "Generation and initial analysis of more than 15,000 full-length human  
 CC RL and mouse cDNA sequences.";  
 CC RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC RN [6]  
 CC RP PROTEIN SEQUENCE OF 38-52.  
 CC RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 CC RA Zhang Z., Henzel W.J.;  
 CC RT "Signal peptide prediction based on analysis of experimentally  
 CC RL verified cleavage sites";  
 CC RL Protein Sci. 13:2819-2824(2004).  
 CC RN [7]  
 CC RP INTERACTIONS WITH CLC AND CNTFR.  
 CC RX MEDLINE=20423191; PubMed=10966616; DOI=10.1038/78765;  
 CC RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H.,  
 CC RA Froger J., Suard I., de Colgnac A.B., Delneste Y., Bonnefoy J.Y.,  
 CC RA Gauchat J.-F., Gaetan H.;  
 CC RT "CLF associates with CLC to form a functional heteromeric ligand for  
 CC RT the CNTF receptor complex.";  
 CC RL Nat. Neurosci. 3:867-872(2000).  
 CC RN [8]  
 CC RP VARIANTS CISS HIS-81 AND ARG-374.  
 CC RX MEDLINE=22428294; PubMed=12509788;  
 CC RA Knappskog P.M., Majewski J., Livneh A., Nilsson P.T.E., Bringasli J.S.,  
 CC RA Ott J., Boman H.;  
 CC RT "Cold-induced sweating syndrome is caused by mutations in the CRLF1  
 CC RT gene.";  
 CC RL Am. J. Hum. Genet. 72:375-383(2003).  
 CC RL -I- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory  
 CC CC role in the immune system and during fetal development. May be  
 CC CC involved in nervous system development.  
 CC CC -I- SUBUNIT: Forms covalently linked di- and tetramers. Forms a  
 CC CC heteromeric complex with cardiotrophin-like cytokine (CLC); the  
 CC CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor  
 CC CC receptor (CNTFR).  
 CC CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC CC -I- TISSUE SPECIFICITY: Highest levels of expression observed in  
 CC CC spleen, thymus, lymph node, appendix, bone marrow, stomach,  
 CC CC placenta, heart, thyroid and ovary. Strongly expressed also in  
 CC CC fetal lung.  
 CC CC -I- INDUCTION: Up-regulated in fibroblast primary cell cultures under  
 CC CC stimulation by IFN-gamma, TNF-alpha and IL-6.  
 CC CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC CC folding and thereby efficient intracellular transport and cell-  
 CC CC surface receptor binding.  
 CC CC -I- DISEASE: Defects in CRLF1 are the cause of cold-induced sweating  
 CC CC syndrome (CISS) [MIM:27430]. CISS is an autosomal recessive  
 CC CC disorder characterized by profuse sweating induced by cool  
 CC CC surroundings (temperatures of 7 to 18 degrees Celsius). Additional  
 CC CC abnormalities include a high-arched palate, nasal voice, depressed  
 CC CC nasal bridge, inability to fully extend the elbows and  
 CC CC kyphoscoliosis.  
 CC CC -I- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3  
 CC CC subfamily.  
 CC CC -I- SIMILARITY: Contains 2 fibronectin type-III domains.

CC CC -I- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
 CC CC domain.  
 CC CC -----  
 CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC CC the European Bioinformatics Institute. There are no restrictions on its  
 CC CC use as long as its content is in no way modified and this statement is not  
 CC CC removed.  
 CC CC -----  
 CC CC EMBL; AF059293; AAC28335.1; -; mRNA.  
 CC CC EMBL; AF073515; AAD39681.1; -; mRNA.  
 CC CC EMBL; AF178684; AAD54385.1; -; mRNA.  
 CC CC EMBL; AY358291; AA088658.1; -; mRNA.  
 CC CC EMBL; BC044634; AAH44634.1; -; mRNA.  
 CC CC HSSP; P40223; 1CD9.  
 CC CC Ensembl; ENSG00000006016; Homo sapiens.  
 CC CC HGNC; HGNC:2364; CRLF1.  
 CC CC MIM; 604237; -.  
 CC CC MIM; 272430; -.  
 CC CC GO; GO:0005615; C:extracellular space; TAS.  
 CC CC GO; GO:0019955; F:cytokine binding; IPI.  
 CC CC GO; GO:0004872; P:receptor activity; TAS.  
 CC CC GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. .); TAS.  
 CC CC InterPro; IPR002996; Cytokn recept\_B/G.  
 CC CC InterPro; IPR003961; FN\_III.  
 CC CC InterPro; IPR007110; Ig-like.  
 CC CC Pfam; PF00041; fn3; 2.  
 CC CC PROSITE; PS50853; FN3; 2.  
 CC CC PROSITE; PS50835; IG LIKE; FALSE NEG.  
 CC CC Direct protein sequencing; Disease mutation; Glycoprotein;  
 CC CC Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.  
 CC KW SIGNAL. 1 37  
 CC FT CHAIN 38 422 Cytokine receptor-like factor 1.  
 CC FT DOMAIN 38 131 Ig-like C2-type.  
 CC FT DOMAIN 134 229 Fibronectin type-III 1.  
 CC FT DOMAIN 234 334 Fibronectin type-III 2.  
 CC FT MOTIF 327 331 WSXWS motif.  
 CC FT MOD\_RES 219 219 Phosphoserine (By similarity).  
 CC FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).  
 CC FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).  
 CC FT CARBOHYD 140 140 N-linked (GlcNAc. .) (Potential).  
 CC FT CARBOHYD 168 168 N-linked (GlcNAc. .) (Potential).  
 CC FT CARBOHYD 292 292 N-linked (GlcNAc. .) (Potential).  
 CC FT CARBOHYD 382 382 By similarity.  
 CC FT DISULFID 143 153 By similarity.  
 CC FT DISULFID 184 195 R -> H (in CISS).  
 CC FT VARIANT 81 81 /FTID=VAR\_017865.  
 CC FT VARIANT 374 374 L -> R (in CISS).  
 CC FT CONFLICT 240 240 /FTID=VAR\_017866.  
 CC FT CONFLICT 240 240 D -> E (in Ref. 3).  
 CC SQ SEQUENCE 422 AA; 46302 MW; AD9DFCB01B84228 CRC64;  
 CC CC Query Match 99.5%; Score 2279.5; DB 1; Length 422;  
 CC CC Best Local Similarity 99.8%; Pred No. 2.4e-166;  
 CC CC Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 CC QY 1 MPAGRRGPAQAQARRPPPLP-LLLLVLGAPRAGSAGHTAVISPDPTLLIGSSLLATC 59  
 CC DB 1 MPAGRRGPAQAQARRPPPLP-LLLLVLGAPRAGSAGHTAVISPDPTLLIGSSLLATC 60  
 CC QY 60 SVHGPPPGATAGLYWTLLNGRLPELSRVLTALANLNGSRQSGDNLVCHARD 119  
 CC DB 61 SVHGPPPGATAGLYWTLLNGRLPELSRVLTALANLNGSRQSGDNLVCHARD 120  
 CC QY 120 GSILAGSLCYGLPPEKPNVISCWKNMDDLTCRWTPGAGHETFLHTNYSKYKLRWYQ 179  
 CC DB 121 GSILAGSLCYGLPPEKPNVISCWKNMDDLTCRWTPGAGHETFLHTNYSKYKLRWYQ 180  
 CC QY 180 DNTCEYHTVGPHSCHIPKDALFTPYEIVWEATNRLGARSVDLTLDLVDVTTDPPPD 239  
 CC DB 181 DNTCEYHTVGPHSCHIPKDALFTPYEIVWEATNRLGARSVDLTLDLVDVTTDPPPD 240

QY 240 VHSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAG 299  
 Db 241 VHSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAG 300  
 QY 300 LKPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTASTPRSRPGPGGACPRGGEPS 359  
 Db 301 LKPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTASTPRSRPGPGGACPRGGEPS 360  
 QY 360 GPVRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDQSGILPSGRGTARGP 419  
 Db 361 GPVRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDQSGILPSGRGTARGP 420  
 QY 420 AR 421  
 Db 421 AR 422

## RESULT 2

ID CRLF1\_MOUSE STANDARD; PRT; 425 AA.  
 AC Q9JW58;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)  
 DE (CLF-1) (Cytokine receptor-like molecule 3) (CRLM-3) (NR6).  
 GN Name=Crlf1; Synonyms=Crlm3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP FUNCTION, AND TISSUE SPECIFICITY.  
 RX PubMed=10359701; DOI=10.1016/S0960-9822(99)80266-8;  
 RA Alexander W.S., Rakar S., Robb L., Farley A., Willson T.A.,  
 RA Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,  
 RA Hasegawa M., Maeda M., Fabril L., Jachno K., Nash A., Metcalf D.,  
 RA Nicola N.A., Hilton D.J.;  
 RT "Suckling defect in mice lacking the soluble haemopoietin receptor  
 NR6.";  
 RL Curr. Biol. 9:605-608(1999).  
 RN [3]  
 RP PHOSPHORYLATION SITE SER-222.  
 RX PubMed=15378723; DOI=10.1002/rcm.1604;  
 RA Jin W.-H., Dai J., Zhou H., Xia Q.-C., Zou H.-F., Zeng R.;  
 RT "Phosphoproteome analysis of mouse liver using immobilized metal  
 affinity purification and linear ion trap mass spectrometry";  
 RL Rapid Commun. Mass Spectrom. 18:2169-2176(2004).  
 CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory  
 CC role in the immune system and during fetal development. May be  
 CC involved in nervous system development (By similarity). Plays an  
 CC essential role in the initiation and/or maintenance of suckling in  
 CC neonatal mice.  
 CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a  
 CC heteromeric complex with cardiotrophin-like cytokine (CLC); the  
 CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor  
 CC receptor (CNTFR) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected  
 CC in the brain of adult mice.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding.  
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)  
 CC domain.

CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; AB040038; BAA92777.1; -; mRNA.  
 DR HSSP; P40223; 1CD9.  
 DR Ensembl; ENSMUSG00000007888; Mus musculus.  
 DR MGI; MGI:1340030; Crlf1.  
 DR CO; CO:0005615; Cextracellular space; TAS.  
 DR InterPro; IPR002996; Cytokn\_recept\_B/G.  
 DR InterPro; IPR003961; FN.III.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS50853; FN3; 2.  
 DR PROSITE; PS50835; IG\_LIKE; FALSE\_NEG.  
 KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;  
 KW Repeat; Signal.  
 FT SIGNAL 1 33 Potential.  
 FT CHAIN 34 425 Cytokine receptor-like factor 1.  
 FT DOMAIN 35 134 Ig-like C2-type.  
 FT DOMAIN 137 232 Fibronectin type-III 1.  
 FT DOMAIN 237 337 Fibronectin type-III 2.  
 FT MOTIF 330 334 WSXWS motif.  
 FT MOD\_RES 222 222 Phosphoserine.  
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 107 107 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 146 156 By similarity.  
 FT DISULFID 187 198 By similarity.  
 SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;  
 Query Match 95.1%; Score 2178; DB 1; Length 425;  
 Best Local Similarity 94.8%; Pred. No. 1.5e-158;  
 Matches 402; Conservative 5; Mismatches 13; Indels 4; Gaps 2;  
 QY 1 MPAGRRGPAQSAARRPP-PLDPL---LLCVLGAPRAGSGAHTAVISPODPTLLIGSSL 56  
 Db 1 MPAGRRGPAQSAARRPPRLSLWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSL 60  
 QY 57 ATCSVHGDPGATAEGLYWTNGRLPPELSVNLASTLALANLNGSRQSGDNLVCH 116  
 Db 61 ATCSVHGDPGATAEGLYWTNGRLPPELSVNLASTLALANLNGSRQSGDNLVCH 120  
 QY 117 ARDGSILAGSCLYVGLPPEKPNISCSNKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176  
 Db 121 ARDGSILAGSCLYVGLPPEKPNISCSNKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180  
 QY 177 YQDNTCEHYTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDELTLIDLVDVTTDP 236  
 Db 181 YQDNTCEHYTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDELTLIDLVDVTTDP 240  
 QY 237 PPDVHVSRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSVDMKVVDVSNQTSR 296  
 Db 241 PPDVHVSRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSVDMKVVDVSNQTSR 300  
 QY 297 LAGLKPVTYFVQVRCNPGIYVSGKAGIWSWSHPTASTPRSRPGPGGACPRGGE 356  
 Db 301 LAGLKPVTYFVQVRCNPGIYVSGKAGIWSWSHPTASTPRSRPGPGGACPRGGE 360  
 QY 357 PSSGPRRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDQSGILPSGRGTA 416  
 Db 361 PSSGPRRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDQSGILPSGRGTA 420  
 QY 417 RGPA 420  
 Db 421 RGPA 424



QY 23 LLLCVGAPRA-CGGAHTAVISPDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRR 81  
 Db 9 LLLLILHSPAVLALSTHVAIVYQDPVLRMGSLTASCWIRSD-LGVHASSLFWTLNGQP 67  
 QY 82 LPPELSRVNASTLALANANGSRQSRGDNLVCHARDGSIILAGSCLYVGLPPEKDVNIS 141  
 Db 68 LPSSLRVLSPTNLSVTLVAGLNASRQTSQDNLVCHHHKGHILAGSCLYVGMPPAKPVNLT 127  
 QY 142 CWSKNKMDLTCRWTPGAHGETFHTNYSKYKLRWYGQDNTCEYHTVGPHSCHIPKOLA 201  
 Db 128 CWSBNTKDLTCSWAPGGRGETHISTQYTLKYKLRWYKECEDYTHVQPYSCSITRDLH 187  
 QY 202 LFTPYEIWEATNRLGASRSDVLTLDILVVTTPDPDVHVSVRVGGLEDQLSVRVWSPPA 261  
 Db 188 LFTPYEIWEASNLGRATSDVITLDILVVTTPDPSPGVTVSVRVGGLEDQLSVRWEAPPA 247  
 QY 262 LKDFLFOAKYQIRYRVESDVWKKVDDVSNQTSCLAGLKPGTVYFVQVRCNPPFGLYGSK 321  
 Db 248 LKDFLFOAKYQIRYRVESDVWKKVDDVSNQTSCLAGLKPGTVYFVQVRCNPPFGLYGSK 307  
 QY 322 KAGINSEWSHPTAASPRSGRPGGACPRGPGSPVRRRLKQFLGWLKHHAY-CS 380  
 Db 308 KAGINSEWSHPTAASPHSER--LMSGSCDSKSSADSNSTLRELKQFFGWVRKHAYGCS 365  
 QY 381 NLSFRLYDQNRAMQKSHKTRNQ 403  
 Db 366 SMSMKLYDQWRVLMQKSHKARNQ 388

## RESULT 5

Q4RMP5\_TETNG  
 ID Q4RMP5\_TETNG PRELIMINARY; PRT; 437 AA.  
 AC Q4RMP5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 10 SCAF15019, whole genome shotgun sequence.  
 DE (Fragment).  
 DE ORFNames=GSTENG00031935001;  
 GN Tetraodon nigroviridis (Green puffer).  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; CAAB01015019; CAG10337.1; -; Genomic\_DNA.  
 DR NON TER 1  
 FT SEQUENCE 437 AA; 49065 MW; 99F9602E88F95583 CRC64;

Query Match 43.4%; Score 994; DB 2; Length 437;  
 Best Local Similarity 53.8%; Pred. No. 9.8e-68;  
 Matches 199; Conservative 33; Mismatches 62; Indels 76; Gaps 5;  
 QY 40 AVISPDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLLPPELSRVNASTLALAL 99  
 Db 1 AVIYQDPVLRMGSLTASCWIRSD-LGVHASSLFWTLNGQPLPSSLYRVLSPTNLSVTL 59  
 QY 100 ANLNGSRQSRGDNLVCHARDGSIILAGSCLYVGLPPEKDVNIS 159  
 Db 60 AGLNASRQTSQDNLVCHHHKGHILAGSCLYVGMPPAKPVNLTCSWNTKDLTCSWAPGGR 119  
 QY 160 GTFTHNTYSLKYKLRWYGQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGSA 219  
 Db 120 GETHISTQYTLKYKLRWYKECEDYTHVQPYSCSITRDLHLFTPYEIWEASNLGRA 179  
 QY 220 RSDVLTLDILVVTTPDPDVHVSVRVGGLEDQLSVRVWSPPAKDFLFOAKYQIRVVED 279  
 Db 180 TSDVITLDILVVTTPDPSPGVTVSVRVGGLEDQLSVRWEAPPAKDFLFOAKYQIRVLED 239  
 QY 280 SYDMK-----VVDD 288  
 Db 240 SQDWKEEKSAFQDERERANTEPLCILGLRVLMNEKYSVEAGPLQMALRLILLPVLVWMD 299  
 QY 289 VSNQTSCLAGLKPGTVYFVQVRCNPPFGLYGSKKAG-----IWSEWSHPTAASPRSGRPG 344  
 Db 300 VGNQTSCLAGLRPGTVYFVQV-----GPRSSASDRIMI-----SDRRV 339  
 QY 345 PGGGACPRG 354  
 Db 340 ASAGPLQPRG 349  
 RESULT 6  
 Q4TCM7\_TETNG  
 ID Q4TCM7\_TETNG PRELIMINARY; PRT; 207 AA.  
 AC Q4TCM7;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF6801, whole genome shotgun sequence.  
 DE (Fragment).  
 DE ORFNames=GSTENG0003230001;  
 GN Tetraodon nigroviridis (Green puffer).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC





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OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast tumor;
RA Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -! DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AF429470; AAM18048.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR SMR; Q87D78; 29-227.
DR Ensemble; ENSG00000113494; Homo sapiens.
DR GO; GO:0016021; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR002996; F:receptor activity; IEA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; HemtreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;

Query Match 14.5%; Score 333; DB 2; Length 268;
Best Local Similarity 36.8%; Pred. No. 2.7e-17;
Matches 83; Conservative 29; Mismatches 97; Indels 18; Gaps 8;

QY 122 ILAGSLCYVG-LPPEKPVNISCSNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQD 180
DB 15 LFNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPDTGG--LPTNYSLTVHREGETLM 72

QY 181 NTCEEYHTVGHPSCHIPKD-LALFTPYEIWEATNRLGARSVDLTLDLVVTTDPPDP 239
DB 73 HECPDYITGPNCHSGFKGQYTSWRTYIMVNATNMGSSFSDELVDVYTVIQDPDPLE 132

QY 240 VHVSRVGGLEDQLSVRWV--SPALKDFF--LFOAKYQIRYRVSDVDMKVVDDVSNQTS 294
DB 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGNTFTLLYEIRLKEKAAEWE-IHFAGQQT 190

QY 295 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPREE 341
DB 191 FKILSLHPGQKYLQVRCRP-----DHGYWSAWSPATFIQIPSGD 230

RESULT 12
Q96P36 HUMAN
ID Q96P36 HUMAN PRELIMINARY; PRT; 288 AA.
AC Q96P36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DE 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolactin receptor short isoform 1b.
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -! DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=11518703;

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RA Hu Z.Z., Meng J., Dufau M.L.;
RT "Isolation and characterization of two novel forms of the human
RT prolactin receptor generated by alternative splicing of a newly
RT identified exon 11.";
RL J. Biol. Chem. 276:41086-41094 (2001).
CC -! DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -! DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AF416618; AAL23914.1; -; mRNA.
DR PIR; B59405; B59405.
DR HSSP; P16471; 1BP3.
DR SMR; Q96P36; 29-227.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; F:receptor activity; IEA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; HemtreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;

Query Match 14.5%; Score 332; DB 2; Length 288;
Best Local Similarity 37.1%; Pred. No. 3.5e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAGSLCYVG-LPPEKPVNISCSNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQD 180
DB 15 LFNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPDTGG--LPTNYSLTVHREGETLM 72

QY 181 NTCEEYHTVGHPSCHIPKD-LALFTPYEIWEATNRLGARSVDLTLDLVVTTDPPDP 239
DB 73 HECPDYITGPNCHSGFKGQYTSWRTYIMVNATNMGSSFSDELVDVYTVIQDPDPLE 132

QY 240 VHVSRVGGLEDQLSVRWV--SPALKDFF--LFOAKYQIRYRVSDVDMKVVDDVSNQTS 294
DB 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGNTFTLLYEIRLKEKAAEWE-IHFAGQQT 190

QY 295 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASP 338
DB 191 FKILSLHPGQKYLQVRCRP-----DHGYWSAWSPATFIQIP 227

RESULT 13
Q9UHJ5 HUMAN
ID Q9UHJ5 HUMAN PRELIMINARY; PRT; 349 AA.
AC Q9UHJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor.";
RL J. Biol. Chem. 274:35461-35468 (1999).
CC -! DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -! DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).

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DR EMBL; AF166329; AAD49855.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR SMR; Q9UHJ5; 29-227.
DR GO; GO:000986; C:cell surface; IDA.
DR GO; GO:0042978; F:ornithine decarboxylase activator activity; NAS.
DR GO; GO:0004925; F:prolactin receptor activity; NAS.
DR GO; GO:0042803; F:protein homodimerization activity; NAS.
DR GO; GO:0006916; P:anti-apoptosis; NAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NAS.
DR GO; GO:0007595; P:lactation; ISS.
DR GO; GO:0006694; P:steroid biosynthesis; NAS.
DR GO; GO:0042110; P:T-cell activation; NAS.
DR GO; GO:0001711; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.
DR InterPro; IPR002996; CytKn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; HemtreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS0853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR KW Receptor.
SQ SEQUENCE 349 AA; 39806 MW; 932F200E850CDD27 CRC64;

Query Match 14.5%; Score 332; DB 2; Length 349;
Best Local Similarity 37.1%; Pred. No. 4.4e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAGSLYVG-LPPEKPNVWSCNMKDLTCRWTPGAGHETFLHTNYSKYLKRWYGD 180
DB 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRGTGG--LPTNYSLTTHREGETLM 72
QY 181 NTCEEVHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSDDLTLDLVVTDPDPPD 239
DB 73 HECPDYITGGPNSCHFGKQYTSWRTYIMMWNATQMGSSFDELYVDVTVYVQDPPPLE 132
QY 240 VHVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVESDVKWVDDVSNQTS 294
DB 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGFTLLYELRLKPKAAWE-IHFAGQQT 190
QY 295 CRLAGLKPGTVYFVQRCNPPFGIYSGKAGIWSHPTAASTP 338
DB 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAWSPATFIQIP 227

RESULT 14
Q96P35 HUMAN
ID Q96P35 HUMAN PRELIMINARY; PRT; 376 AA.
AC Q96P35;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolactin receptor short isoform 1a.
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Hu 2.2., Meng J., Dufau M.L.;
RA PubMed=11518703;
RT "Isolation and characterization of two novel forms of the human
RT prolactin receptor generated by alternative splicing of a newly
RT identified exon 11."
RL J. Biol. Chem. 276:41086-41094(2001).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation (By similarity).
EMBL; AF416619; AAL23915.1; -; mRNA.
FIR; AS9405; AS9405.
HSSP; P16471; 1BP3.
SMR; Q96P35; 29-227.
DR Ensembl; ENSG00000113494; Homo sapiens.
DR GO; GO:000986; C:cell surface; ISS.
DR GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.
DR GO; GO:0004925; F:prolactin receptor activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
DR GO; GO:0007595; P:lactation; ISS.
DR GO; GO:0006694; P:steroid biosynthesis; ISS.
DR GO; GO:0042110; P:T-cell activation; ISS.
DR GO; GO:0001711; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; ISS.
DR InterPro; IPR002996; CytKn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; HemtreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS0853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR KW Receptor.
SQ SEQUENCE 376 AA; 42639 MW; 112DC2555FBC4601 CRC64;

Query Match 14.5%; Score 332; DB 2; Length 376;
Best Local Similarity 37.1%; Pred. No. 4.8e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAGSLYVG-LPPEKPNVWSCNMKDLTCRWTPGAGHETFLHTNYSKYLKRWYGD 180
DB 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRGTGG--LPTNYSLTTHREGETLM 72
QY 181 NTCEEVHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSDDLTLDLVVTDPDPPD 239
DB 73 HECPDYITGGPNSCHFGKQYTSWRTYIMMWNATQMGSSFDELYVDVTVYVQDPPPLE 132
QY 240 VHVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVESDVKWVDDVSNQTS 294
DB 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGFTLLYELRLKPKAAWE-IHFAGQQT 190
QY 295 CRLAGLKPGTVYFVQRCNPPFGIYSGKAGIWSHPTAASTP 338
DB 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAWSPATFIQIP 227

RESULT 15
PRLR_HUMAN
ID PRLR_HUMAN STANDARD; PRT; 622 AA.
AC P16471; Q16354; Q9BX87;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Edery M., Shirota M., Jolicoeur C., Lesueur L., Ali S.,
RA Gould D., Djiane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells."
RL Mol. Endocrinol. 3:1455-1461(1989).

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RN NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RX MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;  
RA Hu Z.-Z., Zhuang L., Meng J., Leonidires M., Dufau M.L.;  
RT "The human prolactin receptor gene structure and alternative promoter  
utilization: the generic promoter hPIII and a novel human promoter  
hp(N).";  
RL J. Clin. Endocrinol. Metab. 84:1153-1156 (1999).  
RN [3]  
RN NUCLEOTIDE SEQUENCE (ISOFORM 2).  
RC TISSUE=Mammary carcinoma;  
RA Kline J.B., Clevenger C.V.;  
RT "Characterization of a novel and functional human prolactin receptor  
isoform (delta-S1 PRLr) containing only one extracellular fibronectin-  
like domain.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RT Kohn M., Ouellette M.J., Utsch W., Lathrop G., Sun J., Winters  
RT Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [5]  
RN PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).  
RC TISSUE=Mammary carcinoma;  
RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;  
RA Fuh G., Wells J.A.;  
RT "Prolactin receptor antagonists that inhibit the growth of breast  
cancer cell lines.";  
RL J. Biol. Chem. 270:13133-13137 (1995).  
RN [6]  
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.  
RX MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;  
RA Somers W., Utsch M., de Vos A.M., Kosiakoff A.A.;  
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";  
RL Nature 372:478-481 (1994).  
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
prolactin.  
CC -!- INTERACTION:  
CC P51956:NEK3; NBExp=1; IntAct=EBI-476182, EBI-476041;  
CC P52735:VAV2; NBExp=1; IntAct=EBI-476182, EBI-297549;  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1;  
CC IsoId=P16471-1; Sequence=Displayed;  
CC Name=2; Synonym=Delta-S1;  
CC IsoId=P16471-2; Sequence=VSP\_001720;  
CC Name=3;  
CC IsoId=P16471-3; Sequence=VSP\_012620, VSP\_012621;  
CC Note=Soluble isoform that appears specific for the BT-474 breast  
cancer cell line;  
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
folding and thereby efficient intracellular transport and cell-  
surface receptor binding.

CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
activation.  
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1  
subfamily.  
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC  
CC EMBL; M31661; AAA60174.1; -; mRNA.  
CC EMBL; AF091870; AAD32032.1; -; Genomic\_DNA.  
CC EMBL; AF091863; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF091864; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF091865; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF091866; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF091867; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF091868; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF091869; AAD32032.1; JOINED; Genomic\_DNA.  
CC EMBL; AF349939; AAK32703.1; -; mRNA.  
CC EMBL; BC059392; AAH59392.1; -; mRNA.  
CC EMBL; S78505; AAB34470.1; -; mRNA.  
CC PIR; A40144; A40144.  
CC PDB; 1BP3; X-ray; B=25-235.  
CC IntAct; P16471; -;  
CC Ensembl; ENSG00000113494; Homo sapiens.  
CC HGNC; HGNC:9446; PRLR.  
CC MIM; 176761; -;  
CC GO; GO:0009986; C:cell surface; IDA.  
CC GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.  
CC GO; GO:0004923; F:prolactin receptor activity; NAS.  
CC GO; GO:0042803; F:protein homodimerization activity; NAS.  
CC GO; GO:0006916; P:anti-apoptosis; NAS.  
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.  
CC GO; GO:0007566; P:embryo implantation; TAS.  
CC GO; GO:0007595; P:lactation; NAS.  
CC GO; GO:0006694; P:steroid biosynthesis; NAS.  
CC GO; GO:0042110; P:T cell activation; NAS.  
CC GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.  
CC GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.  
CC InterPro; IPR002996; Cytokn\_recept\_B/G.  
CC InterPro; IPR003961; FN\_III.  
CC InterPro; IPR003528; HemtreceptL\_F1.  
CC Pfam; PF00041; fn3; 2.  
CC PROSITE; PS00853; FN3; 2.  
CC PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
CC 3D-structure; Alternative splicing; Glycoprotein; Receptor; Repeat;  
KW Signal; Transmembrane.  
KW SIGNAL 1 24  
FT CHAIN 25 622  
FT TOPO\_DOM 25 234  
FT TRANSMEM 235 258  
FT TOPO\_DOM 259 622  
FT DOMAIN 27 121  
FT DOMAIN 127 227  
FT MOTIF 215 219  
FT MOTIF 267 275  
FT CARBOHYD 59 59  
FT CARBOHYD 104 104  
FT CARBOHYD 233 233  
FT DISULFID 36 46  
FT DISULFID 75 86  
FT VARSPLIC 24 124  
FT VARSPLIC 229 230  
FT VARSPLIC 231 622  
FT STRAND 31 38  
FT STRAND 44 50  
FT STRAND 61 66

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FT STRAND 73 74
FT TURN 80 81
FT STRAND 85 88
FT TURN 91 92
FT STRAND 98 106
FT STRAND 112 113
FT STRAND 117 120
FT HELIX 121 123
FT STRAND 125 125
FT STRAND 134 134
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FT TURN 155 156
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SQ SEQUENCE 622 AA; DB7FD0328608C787 CRC64;

Query Match 14.5%; Score 332; DB 1; Length 622;
Best Local Similarity 37.1%; Pred. NO. 9e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAGSCLYVG-LPPEKPVNISCKNMKDLTCBWTGAGHGETFLHNTNYSIKYKLRWYGQD 180
Db 15 LFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWREGTDGG--LPTNYSLTYHREGETLM 72

QY 181 NTCEEYHTVGPBSCHIPKD-LALFPEYIWEATNRLGARSVDLTLDLDVVTTDPPD 239
Db 73 HECPDYITGPNBSCHFGKQYTSWRTYIMVVRATNMGSSFSDELYVDVTYIVQDPPL 132

QY 240 VHSRVYGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYVEDSDVKVDDVSNQTS 294
Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPAAWE-IHFAGQQTE 190

QY 295 CRLAGLKPGTVTVQVRCNPFGLYGSKKAGIWSHPTAATP 338
Db 191 FKILSLHPGQKYLQVRCCKP-----DHGYWSANSPATFIQTP 227
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Search completed: April 11, 2006, 02:16:17  
Job time : 125.397 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 02:16:39 ; Search time 29.0921 Seconds  
(without alignments)  
1196.422 Million cell updates/sec

Title: US-09-037-657-44  
Perfect score: 2290  
Sequence: 1 MPAGRRGPAQAQARRPPPL.....NQDEGLPSRRGTARGPAR 421

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*  
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4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2279.5	99.5	422	2	US-09-866-028-32
2	2279.5	99.5	422	2	US-09-944-457-32
3	2279.5	99.5	422	2	US-09-945-584-32
4	2279.5	99.5	422	2	US-09-944-944-32
5	2279.5	99.5	422	2	US-09-945-587-32
6	2275.5	99.4	422	2	US-09-071-224-2
7	2196	95.9	425	2	US-09-071-224-4
8	2188	95.5	410	2	US-09-521-335-12
9	2165	94.5	425	2	US-09-071-224-6
10	2164.5	94.5	448	2	US-09-120-601-6
11	2109	92.1	405	2	US-09-012-072-2
12	2109	92.1	405	2	US-09-120-601-2
13	2108	92.1	388	2	US-09-071-224-17
14	2095	91.5	407	2	US-09-521-335-13
15	2093.5	91.4	434	2	US-09-012-072-4
16	2093.5	91.4	434	2	US-09-120-601-4
17	2092	91.4	385	2	US-09-071-224-20
18	2045	89.3	385	2	US-09-071-224-19
19	2025	88.4	392	2	US-09-071-224-18
20	2009	87.7	389	2	US-09-071-224-22
21	2008	87.7	389	2	US-09-071-224-28
22	2008	87.7	389	2	US-09-071-224-29
23	2007	87.6	389	2	US-09-071-224-30
24	2006	87.6	389	2	US-09-071-224-24
25	2006	87.6	389	2	US-09-071-224-25
26	2006	87.6	389	2	US-09-071-224-27
27	2005	87.6	389	2	US-09-071-224-26

28	2004	87.5	389	2	US-09-071-224-31	Sequence 31, Appl
29	1645	71.8	303	2	US-09-071-224-23	Sequence 23, Appl
30	1641	71.7	303	2	US-09-071-224-21	Sequence 21, Appl
31	332	14.5	349	2	US-08-806-597A-14	Sequence 14, Appl
32	332	14.5	349	2	US-08-970-428A-14	Sequence 14, Appl
33	332	14.5	637	2	US-09-949-016-10128	Sequence 10128, A
34	329.5	14.4	1168	2	US-09-313-942-24	Sequence 24, Appl
35	329.5	14.4	1168	2	US-10-282-162-24	Sequence 24, Appl
36	325.5	14.2	599	2	US-09-000-145-2	Sequence 2, Appl
37	325	14.2	332	2	US-09-313-942-10	Sequence 10, Appl
38	325	14.2	332	2	US-10-282-162-10	Sequence 10, Appl
39	324.5	14.2	1158	2	US-09-313-942-26	Sequence 26, Appl
40	324.5	14.2	1158	2	US-10-282-162-26	Sequence 26, Appl
41	323	14.1	488	1	US-08-599-455B-5	Sequence 5, Appl
42	323	14.1	488	2	US-09-069-781B-5	Sequence 5, Appl
43	323	14.1	488	2	US-09-137-132-5	Sequence 5, Appl
44	323	14.1	488	2	US-08-864-564A-5	Sequence 5, Appl
45	323	14.1	488	2	US-09-094-410-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-866-028-32  
; Sequence 32, Application US/09866028  
; Patent No. 6642360  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/866,028  
; CURRENT FILING DATE: 2001-05-25  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 32  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-866-028-32

Query Match	99.5%;	Score	2279.5;	DB 2;	Length	422;			
Best Local Similarity	99.8%;	Pred. No.	1.2e-210;						
Matches	421;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
Qy	1	MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC	59						
Db	1	MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC	60						
Qy	60	SVHGDPGPGATAGLYWTNLNRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD	119						
Db	61	SVHGDPGPGATAGLYWTNLNRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD	120						
Qy	120	GSILAGSCLYVGLPPKPKPVNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQG	179						
Db	121	GSILAGSCLYVGLPPKPKPVNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQG	180						

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QY 180 DNTCEYHTVGHPSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDDLVVTTDDPPD 239
Db 181 DNTCEYHTVGHPSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDDLVVTTDDPPD 240
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Db 241 VHSVSRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPFGIYVSKAGIWSWSHPTAATPRSRPPGGGACBPRGEPSS 359
Db 301 LKPGTVYFVQVRCNPFGIYVSKAGIWSWSHPTAATPRSRPPGGGACBPRGEPSS 360
QY 360 GPRVRELKQFLGWLKHKHAYCSNLSRFLYDQWRAWMQKSHKTRNDEGILPSSRRGTARGP 419
Db 361 GPRVRELKQFLGWLKHKHAYCSNLSRFLYDQWRAWMQKSHKTRNDEGILPSSRRGTARGP 420
QY 420 AR 421
Db 421 AR 422

RESULT 2
US-09-944-457-32
; Sequence 32, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
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; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-457-32

Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.2e-210;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVTSPQDPTLLIGSSLLATC 60
QY 60 SVHGDPGPGATAGLYWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
Db 61 SVHGDPGPGATAGLYWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPVNI1SCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYQ 179
Db 121 GSILAGSCLYVGLPPEKPVNI1SCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYQ 180
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Db 181 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDDVVTDDPPD 240  
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QY 300 LKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTPRSRPPGGGACBPRGGEPS 359  
Db 301 LKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTPRSRPPGGGACBPRGGEPS 360  
QY 360 GVPRELKQFLGWLKXKHCYNSLSPRLYDQWAWKQSHKTRNDEGILPSSRGRTARGP 419  
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QY 420 AR 421  
Db 421 AR 422

RESULT 3  
US-09-945-584-32  
; Sequence 32, Application US/09945584  
; Patent No. 6908993  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Batson, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Eileen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,584  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998

QY 100 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDDVVTDDPPD 239  
Db 101 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDDVVTDDPPD 240  
QY 240 VHSVSVGGLEDQLSVRWSPALKDPLFOAKQIRYRVEDSVDWKVVDDVSNQTSCLAG 299  
Db 241 VHSVSVGGLEDQLSVRWSPALKDPLFOAKQIRYRVEDSVDWKVVDDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTPRSRPPGGGACBPRGGEPS 359  
Db 301 LKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTPRSRPPGGGACBPRGGEPS 360  
QY 360 GVPRELKQFLGWLKXKHCYNSLSPRLYDQWAWKQSHKTRNDEGILPSSRGRTARGP 419  
Db 361 GVPRELKQFLGWLKXKHCYNSLSPRLYDQWAWKQSHKTRNDEGILPSSRGRTARGP 420  
QY 420 AR 421  
Db 421 AR 422

Query Match 99.5%; Score 2279.5; DB 2; Length 422;  
Best Local Similarity 99.8%; Pred. No. 1.2e-210;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MPAGRGPAAGSARRPPPLP-LIALLCVLGAPRAGSGAHTAVISPDPTLLIGSSILATC 59  
Db 1 MPAGRGPAAGSARRPPPLP-LIALLCVLGAPRAGSGAHTAVISPDPTLLIGSSILATC 60  
QY 60 SVHGDPPGATAGLYWTNLNGRLPPELSRVNLASTLALANLNGSRQSGDNLVCHARD 119  
Db 61 SVHGDPPGATAGLYWTNLNGRLPPELSRVNLASTLALANLNGSRQSGDNLVCHARD 120  
QY 120 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLKYKLRWYQ 179  
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[illegible]

## RESULT 4

US-09-944-944-32  
; Sequence 32, Application US/09944944  
; Patent No. 6929947  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerlitsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,944  
; PRIORITY FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998

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Db 181 DNTCEYHTVGHSHCHIPKDLALFTPEYEWVEATNRLGARSVDLTLDILDVVTDDPPD 240  
QY 240 VHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 299  
Db 241 VHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 300  
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Db 301 LKPGTVFYVQVRCNPGFIYGSCKAGIWSWSHPTAASTPRSRPGRGGACBPRGGEPS 360  
QY 360 GPVRELKQFLGWLKHCAYCSNLSFRLYDQWRAWMQSHKTRNQDGIILPSSRRGTARGP 419  
Db 361 GPVRELKQFLGWLKHCAYCSNLSFRLYDQWRAWMQSHKTRNQDGIILPSSRRGTARGP 420  
QY 420 AR 421  
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RESULT 5

US-09-945-587-32  
; Sequence 32, Application US/09945587  
; Patent No. 6936254  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavlin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tomas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,587  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/1146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6936254ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6936254ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 32  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-945-587-32

Query Match 99.5%; Score 2279.5; DB 2; Length 422;  
Best Local Similarity 99.8%; Pred. No. 1.2e-210;  
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MPAGRRGPAQAQARRPPPLLP-LLLLCVLGAPRAGSGAHTAVTSPQDPTLLIGSSLLATC 59  
Db 1 MPAGRRGPAQAQARRPPPLLP-LLLLCVLGAPRAGSGAHTAVTSPQDPTLLIGSSLLATC 60  
QY 60 SVHGDPGATAGLYWTNLNGRELPPELSRVLTALALANLNGSRQSGDNLVCHARD 119  
Db 61 SVHGDPGATAGLYWTNLNGRELPPELSRVLTALALANLNGSRQSGDNLVCHARD 120  
QY 120 GSILAGSCLYVCLPPEKPVNISCWNKMDLTCRWTPGAHGETFLHTNYSLKVKLRWYQG 179  
Db 121 GSILAGSCLYVGLPPEKPVNISCWNKMDLTCRWTPGAHGETFLHTNYSLKVKLRWYQG 180

QY 180 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLILDVTTDPPD 239  
DB 181 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLILDVTTDPPD 240  
QY 240 VHSVVGGLDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 299  
DB 241 VHSVVGGLDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGACPRGEPSS 359  
DB 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGACPRGEPSS 360  
QY 360 GVPRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 419  
DB 361 GVPRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 420  
QY 420 AR 421  
DB 421 AR 422

## RESULT 6

US-09-071-224-2

; Sequence 2, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Gelmbert, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 422 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal

US-09-071-224-2

Query Match

99.4%; Score 2275.5; DB 2; Length 422;

Best Local Similarity 99.5%; Pred. No. 2.9e-210;  
Matches 420; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MPAGRGPAQASARRPPPLP-LLLL CVLGAPRAGSGAHTAVISPDPTLLIGSLLATC 59  
DB 1 MPAGRGPAQASARRPPPLP-LLLL CVLGAPRAGSGAHTAVISPDPTLLIGSLLATC 60  
QY 60 SVHGDPPGATAGELYWTNLNGRRLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 119  
DB 61 SVHGDPPGATAGELYWTNLNGRRLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120  
QY 120 GSILAGSCLYVGLPEKPNISCSKMKDLCRTWTPGAHGETFLHTNYSKYKLRWYQ 179  
DB 121 GSILAGSCLYVGLPEKPNISCSKMKDLCRTWTPGAHGETFLHTNYSKYKLRWYQ 180  
QY 180 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLILDVTTDPPD 239  
DB 181 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLILDVTTDPPD 240  
QY 240 VHSVVGGLDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 299  
DB 241 VHSVVGGLDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGACPRGEPSS 359  
DB 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPTAASPRSRPFGGACPRGEPSS 360  
QY 360 GVPRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 419  
DB 361 GVPRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 420  
QY 420 AR 421  
DB 421 AR 422

## RESULT 7

US-09-071-224-4  
; Sequence 4, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Gelmbert, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 422 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal

US-09-071-224-4

Query Match

99.4%; Score 2275.5; DB 2; Length 422;

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-071-224-4

Query Match 95.9%; Score 2196; DB 2; Length 425;  
Best Local Similarity 100.0%; Pred. No. 1.3e-202;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRRGPAQAARRPPPLP LLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS 60  
DB 1 MPAGRRGPAQAARRPPPLP LLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS 60  
QY 61 VHGDPGATAGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120  
DB 61 VHGDPGATAGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120  
QY 121 SILAGSCLVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSLKYLRYWGQD 180  
DB 121 SILAGSCLVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSLKYLRYWGQD 180  
QY 181 NTCEEYHTVGPCHSCHIPKD LALFTPYEIWEATNRLGARSVDLTLDLDVVTTDPPPDV 240  
DB 181 NTCEEYHTVGPCHSCHIPKD LALFTPYEIWEATNRLGARSVDLTLDLDVVTTDPPPDV 240  
QY 241 HVSRVGGLDQLSVRWVSPALDKFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAGL 300  
DB 241 HVSRVGGLDQLSVRWVSPALDKFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAGL 300  
QY 301 KPGTVYFVQVRCNPFGIYSGKKAGIWSHSHPTAASTPRSERPGGACPRGGPSSG 360  
DB 301 KPGTVYFVQVRCNPFGIYSGKKAGIWSHSHPTAASTPRSERPGGACPRGGPSSG 360  
QY 361 PVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ 403  
DB 361 PVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ 403

RESULT 8

US-09-521-335-12  
Sequence 12, Application US/09521335  
Patent No. 6800460  
GENERAL INFORMATION:  
APPLICANT: Oppmann, Birgit  
APPLICANT: Timans, Jacqueline C.  
APPLICANT: Kastelein, Robert A.  
APPLICANT: Bazan, J. Fernando  
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
FILE REFERENCE: DX0935K  
CURRENT APPLICATION NUMBER: US/09/521,335  
CURRENT FILING DATE: 2000-03-09  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 410  
TYPE: PRT  
ORGANISM: primate  
US-09-521-335-12

Query Match 95.5%; Score 2188; DB 2; Length 410;  
Best Local Similarity 98.8%; Pred. No. 7.3e-202;  
Matches 405; Conservative 1; Mismatches 0; Indels 4; Gaps 2;

QY 1 MPAGRRGPAQAARRPPPLP LLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 59

DB 1 MPAGRRGPAQAARRPPPLP LLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60  
QY 60 SVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119  
DB 61 SVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120  
QY 120 GSILAGSCLVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSLKYLRYWGQ 179  
DB 121 GSILAGSCLVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSLKYLRYWGQ 180  
QY 180 DNTCEEYHTVGPCHSCHIPKD LALFTPYEIWEATNRLGARSVDLTLDLDVVTTDPPPD 239  
DB 181 DNTCEEYHTVGPCHSCHIPKD LALFTPYEIWEATNRLGARSVDLTLDLDVVTTDPPPD 240  
QY 240 HVSRVGGLDQLSVRWVSPALDKFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAG 299  
DB 241 HVSRVGGLDQLSVRWVSPALDKFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAG 300  
QY 300 LKPGTVYFVQVRCNPFGIYSGKKAGIWSHSHPTAASTPRSERPGGACPRGGPSS 359  
DB 301 LKPGTVYFVQVRCNPFGIYSGKKAGIWSHSHPTAASTPRSERPGGACPRGGPSS 360  
QY 360 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDREGILP 409  
DB 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ ---VLP 407

RESULT 9

US-09-071-224-6  
Sequence 6, Application US/09071224  
Patent No. 6271343  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Presnell, Scott R.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Gilbert, Teresa  
APPLICANT: Foster, Donald C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Lehner, Joyce M.  
TITLE OF INVENTION: MAMMALIAN ZCYTORS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESS: Zymogenetics  
STREET: 1201 Eastlake Ave East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,224  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 amino acids  
TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-6

Query Match          94.5%; Score 2165; DB 2; Length 425;
Best Local Similarity 94.1%; Pred. No. 1.3e-199;
Matches 399; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

QY 1 MPAGRRGPAQAARRPP-----PLLPLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 56
Db 1 MPAGGPGPAQAARRPPRLSSLLCVLGVQGGSGAHTAVISPODPTLLIGSSLLH 60

QY 57 ATCSVHGDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCH 116
Db 61 ATCSIHGDTPGATAGLYWTLNGRRLLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 117 ARDGSILAGSCLYVGLPPEKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176
Db 121 ARDGSILAGSCLYVGLPPEKPVNISCSWRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 177 YGQDNTCEYHVTGPHSCHIPKDLALFTPEYIWEATNRLSGARSVDLFLDLDVVTTDP 236
Db 181 YQDNTCEYHVTGPHSCHIPKDLALFTPEYIWEATNRLSGARSVDLFLDLDVVTTDP 240

QY 237 PPDVHVSRYGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSDVKVVDVSNQTSR 296
Db 241 PPDVHVSRYGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDSDVKVVDVSNQTSR 300

QY 297 LAGLKPGTVYFQVRCNPFGIYGSKKAGIWESEWSPHTAASPRSERPGGGACPRGGE 356
Db 301 LAGLKPGTVYFQVRCNPFGIYGSKKAGIWESEWSPHTAASPRSERPGGGVCEPRGGE 360

QY 357 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMOKSHKTRNQDREGILPSGRGTA 416
Db 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMOKSHKTRNQDREGILPSGRGTA 420

QY 417 RGPA 420
Db 421 RGPA 424

RESULT 10
US-09-120-601-6
; Sequence 6, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 448
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-6

Query Match          94.5%; Score 2164.5; DB 2; Length 448;
Best Local Similarity 94.6%; Pred. No. 1.5e-199;
Matches 403; Conservative 0; Mismatches 0; Indels 23; Gaps 2;

QY 1 MPAGRRGPAQAARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 59
Db 1 MPAGRRGPAQAARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60

QY 60 SVHGDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
Db 60 SVHGDPPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120

QY 120 GSILAGSCLYVGLPPEKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQO 179
Db 121 GSILAGSCLYVGLPPEKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQO 180

QY 180 DNTCEYHVTGPHSCHIPKDLALFTPEYIWEATNRLSGARSVDLFLDLD----- 230
Db 181 DNTCEYHVTGPHSCHIPKDLALFTPEYIWEATNRLSGARSVDLFLDLDVGSHLPLPS 240

QY 231 -----VTTDPPDVHVSRYGGLEDQLSVRWSPPALKDFLFOAKYQIRYRV 277
Db 241 PATPGLSLLVRGKVTTDPPDVHVSRYGGLEDQLSVRWSPPALKDFLFOAKYQIRYRV 300

QY 278 EDSVDWKVDDVSNQTSRLAGLKPGTVYFQVRCNPFGIYGSKKAGIWESEWSPHTAAS 337
Db 301 EDSVDWKVDDVSNQTSRLAGLKPGTVYFQVRCNPFGIYGSKKAGIWESEWSPHTAAS 360

QY 338 PRSBRPGGGACPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMOKS 397
Db 361 PRSBRPGGGACPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMOKS 420

QY 398 HKTRNQ 403
Db 421 HKTRNQ 426

RESULT 11
US-09-012-072-2
; Sequence 2, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-012-072-2

Query Match          92.1%; Score 2109; DB 2; Length 405;
Best Local Similarity 96.5%; Pred. No. 2.9e-194;
Matches 384; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 23 LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRLL 82
Db 7 LLLCVLGPRGGSGAHTAVISPODPTLLIGSSLLQATCSIHGDTPGATAGLYWTLNGRRLL 66

QY 83 PPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEKPVNIS 142
Db 67 PSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEKPVNIS 126

QY 143 WSKNMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHVTGPHSCHIPKDLAL 202
Db 127 WSRNMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHVTGPHSCHIPKDLAL 186

QY 203 FPTYEIWEATNRLSGARSVDLFLDLDVVTTDPPDVHVSRYGGLEDQLSVRWSPPAL 262
Db 187 FPTYEIWEATNRLSGARSVDLFLDLDVVTTDPPDVHVSRYGGLEDQLSVRWSPPAL 246

QY 263 KDFLFOAKYQIRYRVEDSDVKVDDVSNQTSRLAGLKPGTVYFQVRCNPFGIYGSKK 322
Db 247 KDFLFOAKYQIRYRVEDSDVKVDDVSNQTSRLAGLKPGTVYFQVRCNPFGIYGSKK 306

QY 323 AGIWESEWSPHTAASPRSERPGGGACPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNL 382
Db 307 AGIWESEWSPHTAASPRSERPGGGVCEPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNL 366
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QY 383 SFRLYDQWRAMQKSHKTRNDEGILPSGRRGTARGPA 420  
Db 367 SFRLYDQWRAMQKSHKTRNDEGILPSGRRGTARGPA 404

## RESULT 12

US-09-120-601-2  
; Sequence 2, Application US/09120601  
; Patent No. 6207413  
; GENERAL INFORMATION:  
; APPLICANT: Masakowski, Piotr  
; TITLE OF INVENTION: No. 6207413el Orphan Receptors  
; FILE REFERENCE: REG 630  
; CURRENT APPLICATION NUMBER: US/09/120,601  
; CURRENT FILING DATE: 1998-07-22  
; EARLIER APPLICATION NUMBER: 09/012,072  
; EARLIER FILING DATE: 1998-01-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 405  
; TYPE: PRT  
; ORGANISM: MOUSE  
US-09-120-601-2

Query Match 92.1%; Score 2109; DB 2; Length 405;  
Best Local Similarity 96.5%; Pred. No. 2.9e-194;  
Matches 384; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 23 LLLCVLGPRAGSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTLLNGRRL 82  
Db 7 LLLCVLGPRGSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTLLNGRRL 66  
QY 83 PPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISC 142  
Db 67 PSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISC 126  
QY 143 WSKNNKMDLTCTWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLAL 202  
Db 127 WSRNKMMDLTCTWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLAL 186  
QY 203 FTPYIWEATNRLGASRSDVLTDLVDTTDPDPPDVHVSVRVGLPQLSVRWVSPPAL 262  
Db 187 FTPYIWEATNRLGASRSDVLTDLVDTTDPDPPDVHVSVRVGLPQLSVRWVSPPAL 246  
QY 263 KDFLFOAKYQIRYVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFGLYGSKK 322  
Db 247 KDFLFOAKYQIRYVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFGLYGSKK 306  
QY 323 AGIWESEWSHPTAASPRSERPGGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNL 382  
Db 307 AGIWESEWSHPTAASPRSERPGGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNL 366  
QY 383 SFRLYDQWRAMQKSHKTRNDEGILPSGRRGTARGPA 420  
Db 367 SFRLYDQWRAMQKSHKTRNDEGILPSGRRGTARGPA 404

## RESULT 13

US-09-071-224-17  
; Sequence 17, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Jeilberg, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 388 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-071-224-17

Query Match 92.1%; Score 2108; DB 2; Length 388;  
Best Local Similarity 99.5%; Pred. No. 3.4e-194;  
Matches 386; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 34 GSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTLLNGRRLPPELSRVLNAS 93  
Db 1 GSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTLLNGRRLPPELSRVLNAS 60  
QY 94 TLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISCWKNMDLTCTR 153  
Db 61 TLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISCWKNMDLTCTR 120  
QY 154 WTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLALFTPYEIVWEAT 213  
Db 121 WTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLALFTPYEIVWEAT 180  
QY 214 NRLGASRSDVLTDLVDTTDPDPPDVHVSVRVGLPQLSVRWVSPPALKDFLFOAKYQI 273  
Db 181 NRLGASRSDVLTDLVDTTDPDPPDVHVSVRVGLPQLSVRWVSPPALKDFLFOAKYQI 240  
QY 274 RYRVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFGLYGSKKAGIWESEWSHPT 333  
Db 241 RYRVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFGLYGSKKAGIWESEWSHPT 300  
QY 334 AASTPRSERPGGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNLSPRLYDQWRAM 393  
Db 301 AASTPRSERPGGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNLSPRLYDQWRAM 360  
QY 394 MOKSHKTRNDEGILPSGRRGTARGPAR 421  
Db 361 MOKSHKTRNDEGILPSGRRGTARGPAR 388

## RESULT 14

US-09-521-335-13  
; Sequence 13, Application US/09521335  
; Patent No. 6800460  
; GENERAL INFORMATION:

```

; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-09-521-335-13

Query Match          91.5%; Score 2095; DB 2; Length 407;
Best Local Similarity 95.1%; Pred. No. 6.4e-193;
Matches 386; Conservative 5; Mismatches 11; Indels 4; Gaps 2;

QY 18 PLLPL---LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGLY 74
   |||||
Db 2 PLSSLSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLLATCSIHGDTFCATAEGLY 61
   |||||

QY 75 WTNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPP 134
   |||||
Db 62 WTNGRRL--PSLSRLANTSTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPP 120
   |||||

QY 135 EKPVNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP 194
   |||||
Db 121 EKPVNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP 180
   |||||

QY 195 HIPKDLALFTPYEIWEATNRLGARSVDLTLDVVTDDPPDVHVSRVGGLDQLSV 254
   |||||
Db 181 HIPKDLALFTPYEIWEATNRLGARSVDLTLDVVTDDPPDVHVSRVGGLDQLSV 240
   |||||

QY 255 RVVSPALKDFLEQAKYQIRYRVESVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCNP 314
   |||||
Db 241 RVVSPALKDFLEQAKYQIRYRVESVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCNP 300
   |||||

QY 315 FGIGSKKAGIWESEWHPHTAASPTPRSERPGGACPRGGBSPVRRRLKQFLGWLK 374
   |||||
Db 301 FGIGSKKAGIWESEWHPHTAASPTPRSERPGGACPRGGBSPVRRRLKQFLGWLK 360
   |||||

QY 375 KHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPSGRGTARGPA 420
   |||||
Db 361 KHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPSGRGTARGPA 406
   |||||

RESULT 15
US-09-012-072-4
; Sequence 4, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-012-072-4

Query Match          91.4%; Score 2093.5; DB 2; Length 434;
Best Local Similarity 94.4%; Pred. No. 9.9e-193;
Matches 389; Conservative 0; Mismatches 0; Indels 23; Gaps 2;

QY 15 RPPPLLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGL 73
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Db 1 RPPPLLP-LLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGL 60
QY 74 YWTLNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLP 133
   |||||
Db 61 YWTLNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLP 120
   |||||
QY 134 PEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP 193
   |||||
Db 121 PEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP 180
   |||||
QY 194 CHIPKDLALFTPYEIWEATNRLGARSVDLTLDL-----V 231
   |||||
Db 181 CHIPKDLALFTPYEIWEATNRLGARSVDLTLDLVDGSHLPLPSPATPGLSLLVRGV 240
   |||||
QY 232 VTTDPPPDVHVSRVGGLDQLSVRVVSPALKDFLEQAKYQIRYRVESVDWKVDDVSN 291
   |||||
Db 241 VTTDPPPDVHVSRVGGLDQLSVRVVSPALKDFLEQAKYQIRYRVESVDWKVDDVSN 300
   |||||
QY 292 QTSCLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESEWHPHTAASPTPRSERPGG 351
   |||||
Db 301 QTSCLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESEWHPHTAASPTPRSERPGG 360
   |||||
QY 352 PRGGEPSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ 403
   |||||
Db 361 PRGGEPSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ 412
   |||||

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Search completed: April 11, 2006, 02:19:00  
Job time : 30.0921 secs

76560  
STIC-Biotech/ChemLib

184613

119

From: Woodward, Michael  
Sent: Friday, April 07, 2006 1:46 PM  
To: STIC-Biotech/ChemLib  
Cc: Hamud, Fozia  
Subject: FW: rush search 09/037, 657

Please put in ~~rush~~ queue.

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APR - 7 2006  
STIC

-----Original Message-----

From: Hamud, Fozia  
Sent: Friday, April 07, 2006 1:38 PM  
To: Woodward, Michael  
Cc: Chan, Christina  
Subject: rush search 09/037, 657

Hi Mr. Woodward,  
Would you kindly approve this rush search? It is a very old case in my docket. The claims are allowable. However, Applicant is running out of time by Thursday the 13th of April. An interference search must be done before then. thanks.

Stic:  
Kindly search SEQ ID NOs: 13, 15 and 44 of 09/037,657 against commercial and interference data bases. Thank you very much.

FOZIA HAMUD  
PATENT EXAMINER  
ART UNIT 1647  
ROOM:REM 4D64  
MAIL BOX: REM 4C70

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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